

78243

192677

m9

STIC-Biotech/ChemLib

From: Jiang, Dong
Sent: Monday, June 12, 2006 6:34 PM
To: STIC-Biotech/ChemLib
Subject: 10/797,157

Please search SEQ ID NO:2 (aa, standard & oligomer search)

- issued & Pub.
- commercial

Please send results on paper to Dong Jiang in REM 4D70 (mail stop REM 4C70).

Thank you very much.

Dong

Dong Jiang

AU1646
REM - 4D70
571-272-0872
Mail stop REM - 4C70

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIS: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

THIS PAGE BLANK (USPTO)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2006, 04:21:48 ; Search time 294.055 Seconds
(without alignments)
293.870 Million cell updates/sec

Title: US-10-797-157-2
Perfect score: 1004
Sequence: 1 MLGSRVLLLLPWTQGR.....QAFVAVARVFAHGAATLSP 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq 8:
1: Geneseqp1980s:
2: Geneseqp1990s:
3: Geneseqp2000s:
4: Geneseqp2001s:
5: Geneseqp2002s:
6: Geneseqp2003as:
7: Geneseqp2003bs:
8: Geneseqp2004s:
9: Geneseqp2005s:
10: Geneseqp2006s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1004	100.0	189	2 AAW95002	Aaw95002 Human int
2	1004	100.0	189	2 AAY29783	Aay29783 Human int
3	1004	100.0	189	3 AAB01981	Aab01981 Human int
4	1004	100.0	189	4 AAB47120	Aab47120 Human IL-
5	1004	100.0	189	6 ABU08268	Abu08268 Human int
6	1004	100.0	189	6 ABG75811	Abg75811 Human int
7	1004	100.0	189	7 ADF70612	Adf70612 Human int
8	1004	100.0	189	8 ADQ14469	Adq14469 Human int
9	1004	100.0	189	8 ADS73601	Ads73601 Human IL-
10	1004	100.0	189	9 ADV98151	Adv98151 Human pl9
11	1004	100.0	189	9 AEA51094	Aea51094 Human int
12	1004	100.0	189	9 AEB47331	Aeb47331 Human int
13	1000	99.6	189	3 AAY94966	Aay94966 Human sec
14	1000	99.6	189	3 AAY54606	Aay54606 SGRF prot
15	1000	99.6	189	4 AAU12287	Aau12287 Human PRO
16	1000	99.6	189	4 AAB48070	Aab48070 Human ext
17	1000	99.6	189	6 AB017731	Ab017731 Novel hum
18	1000	99.6	189	6 ABU80985	Abu80985 Human PRO
19	1000	99.6	189	6 ABU66685	Abu66685 Human PRO
20	1000	99.6	189	6 ABU59766	Abu59766 Novel sec
21	1000	99.6	189	6 ABO24956	Abo24956 Human sec
22	1000	99.6	189	6 ABU66961	Abu66961 Human sec
23	1000	99.6	189	6 ADA45751	Ada45751 Novel hum

24	1000	99.6	189	6 ADA76182	Ada76182 Human PRO
25	1000	99.6	189	6 ADA18832	Ada18832 Human PRO
26	1000	99.6	189	6 ADA61455	Ada61455 Homo sapi
27	1000	99.6	189	6 ADB19240	Adb19240 Novel hum
28	1000	99.6	189	6 ADB27781	Adb27781 Human PRO
29	1000	99.6	189	6 ADA86260	Ada86260 Novel hum
30	1000	99.6	189	6 ADB15824	Adb15824 Human PRO
31	1000	99.6	189	6 ADA47610	Ada47610 Human PRO
32	1000	99.6	189	6 ADA67405	Ada67405 Human PRO
33	1000	99.6	189	6 ADB30412	Adb30412 Human PRO
34	1000	99.6	189	6 ADA85708	Ada85708 Novel hum
35	1000	99.6	189	6 ADA96920	Ada96920 Human PRO
36	1000	99.6	189	6 ADA79224	Ada79224 Human PRO
37	1000	99.6	189	6 ADA87363	Ada87363 Novel hum
38	1000	99.6	189	6 ADB16565	Adb16565 Human PRO
39	1000	99.6	189	6 ADA91557	Ada91557 Novel hum
40	1000	99.6	189	6 ADB14720	Adb14720 Human PRO
41	1000	99.6	189	6 ADB18681	Adb18681 Novel hum
42	1000	99.6	189	6 ADA93896	Ada93896 Human PRO
43	1000	99.6	189	6 ADB19792	Adb19792 Novel hum
44	1000	99.6	189	6 ADB13104	Adb13104 Human PRO
45	1000	99.6	189	6 ABO43264	Abo43264 Novel hum

ALIGNMENTS

RESULT 1
AAW95002
ID AAW95002 standard; protein; 189 AA.
XX
AC AAW95002;
XX
DT 21-MAY-1999 (first entry)
XX
DE Human interleukin-B30 (IL-B30) polypeptide.
XX
KW Cytokine; interleukin-B30; IL-B30; forensic science; cell proliferation; inflammatory condition; drug screening; human.
XX
OS Homo sapiens.
XX
FH Key
FT Peptide
FT Protein
FT Protein
XX
PN WO9905280-A1.
XX
PD 04-FEB-1999.
XX
PF 24-JUL-1998; 98WO-US015423.
XX
PR 25-JUL-1997; 97US-00900905.
XX
SC (SCHE) SCHERING CORP.
XX
BZ Bazan JF;
XX
WP 1999-142935/12.
XX
N-PSDB; AAX17786.
XX
PT Newly isolated or recombinant polynucleotide encoding mammalian cytokine interleukin-B30 (IL-B30), including fragments - useful for regulating activation, development, differentiation and function of various cell types, and for diagnosing and treating conditions associated with IL-B30.
XX
PS Claim 2; Page 8-9; 83pp; English.
XX
CC This represents a human cytokine interleukin-B30 (IL-B30) polypeptide. Host cells containing a vector comprising the IL-B30 nucleic acid are used for the recombinant production of the protein. The polynucleotides

CC are useful for diagnosis of IL-B30 mediated conditions, and forensic
 CC science (e.g. to distinguish rodent from human, or as a marker to
 CC distinguish between different cells exhibiting differential expression or
 CC modification patterns). The IL-B30 (including fragments), together with
 CC antibodies that bind to IL-B30 are useful for teaching purposes. They are
 CC also used for treating conditions associated with abnormal physiology or
 CC development, including inflammatory conditions. The polypeptide cytokine
 CC should mediate cytokine synthesis and proliferation in cells. IL-B30 is
 CC useful for drug screening to identify compounds having binding affinity
 CC to IL-B30
 XX
 SQ Sequence 189 AA;

Query Match 100.0%; Score 1004; DB 2; Length 189;
 Best Local Similarity 100.0%; Pred. No. 6.2e-97;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGSRVAMLLLLPWTAAQGRAVPGSSPAWTCQQLSQKLTCLAWSAHPLVGHMDLREEG 60
 DB 1 MLGSRVAMLLLLPWTAAQGRAVPGSSPAWTCQQLSQKLTCLAWSAHPLVGHMDLREEG 60
 QY 61 DEETTNDVPHIQCGDGPQGLRDNSQFCQRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120
 DB 61 DEETTNDVPHIQCGDGPQGLRDNSQFCQRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120
 QY 121 VAQLHASLLGLSOLLOPEGHWHWETQIPSLSPSQPWQRLRLRPKILRSLOAFVAAARVF 180
 DB 121 VAQLHASLLGLSOLLOPEGHWHWETQIPSLSPSQPWQRLRLRPKILRSLOAFVAAARVF 180
 QY 181 AHGAATLSP 189
 DB 181 AHGAATLSP 189

RESULT 2
 AAY29783
 ID AAY29783 standard; protein; 189 AA.
 XX
 AC AAY29783;
 DT 04-NOV-1999 (first entry)
 XX Human interleukin B30.
 DE
 XX DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;
 KW interleukin B30; DCRS1; IL-B30; cytokine receptor; diagnosis;
 KW inflammatory disorder; inflammatory response; innate immunity;
 KW morphogenic development; immunological disorder.
 XX

OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..21
 FT /label= signal
 FT Protein 22..189
 FT /label= IL-B30
 XX
 FN WO9940195-A1.
 XX
 PD 12-AUG-1999.
 XX
 PF 05-FEB-1999; 99MO-US002600.
 XX
 PR 06-FEB-1998; 98US-0073941P.
 PR 13-MAY-1998; 98US-00078194.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 FI Mattson JD, Mcclanahan TK, Kastelein RA;
 XX
 DR WPI; 1999-527306/44.
 DR N-PSDB; AAZ08865.
 XX

PT New receptor subunits useful in the treatment inflammatory disorders.
 XX
 PS Claim 2; Page 26-27; 133pp; English.
 XX
 CC The present invention describes a composition (I) comprising DNAX
 CC cytokine receptor subunit I (DCRS1) protein and DNAX soluble receptor
 CC subunit I (DSRS1) protein, which together encode a new mammalian cytokine
 CC -related receptor (R), or DCRS1 and interleukin B30 (IL-B30) proteins, or
 CC DRS1 and IL-B30 proteins. (I) comprising DRS1 and DCRS1 is useful for
 CC screening for ligands (i.e. agonists/antagonists) from a library of
 CC compounds, which are useful for modulating the physiology or development
 CC of a cell or tissue culture e.g. inflammatory responses, innate immunity
 CC and/or morphogenic development. (R), antibodies and ligands are useful
 CC for treatment of conditions, especially immunological disorders,
 CC associated with conditions exhibiting abnormal expression of (R). (R) is
 CC useful as a phosphate labeling enzyme to label substrates, and the
 CC subunits DRS1 and DCRS1 are useful as immunogens for generating
 CC antibodies, or as antigens for binding antibodies. Nucleic acids encoding
 CC (R) are useful for identifying related DNAs and mRNAs, and variants from
 CC other individuals or species. The present sequence represents the
 CC specifically claimed human IL-B30, for use in the composition of the
 CC present invention
 XX
 SQ Sequence 189 AA;

Query Match 100.0%; Score 1004; DB 2; Length 189;
 Best Local Similarity 100.0%; Pred. No. 6.2e-97;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGSRVAMLLLLPWTAAQGRAVPGSSPAWTCQQLSQKLTCLAWSAHPLVGHMDLREEG 60
 DB 1 MLGSRVAMLLLLPWTAAQGRAVPGSSPAWTCQQLSQKLTCLAWSAHPLVGHMDLREEG 60
 QY 61 DEETTNDVPHIQCGDGPQGLRDNSQFCQRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120
 DB 61 DEETTNDVPHIQCGDGPQGLRDNSQFCQRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120
 QY 121 VAQLHASLLGLSOLLOPEGHWHWETQIPSLSPSQPWQRLRLRPKILRSLOAFVAAARVF 180
 DB 121 VAQLHASLLGLSOLLOPEGHWHWETQIPSLSPSQPWQRLRLRPKILRSLOAFVAAARVF 180
 QY 181 AHGAATLSP 189
 DB 181 AHGAATLSP 189

RESULT 3
 AAB01981
 ID AAB01981 standard; protein; 189 AA.
 XX
 AC AAB01981;
 DT 27-SEP-2000 (first entry)
 XX Human interleukin-B30 (IL-B30).
 DE
 XX Interleukin-B30; IL-B30; human; cytokine; cellular signalling;
 KW immune response; haematopoietic cell; IL-6 homologue; GCSF homologue;
 KW granulocyte colony stimulating factor; immune disorder;
 KW inflammatory disease; autoimmune disease; antigen; antibody.
 XX

OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..21
 FT /note= "Signal peptide"
 FT Protein 22..189
 FT /note= "Mature human IL-B30"
 XX
 XX US6060284-A.
 XX
 PD 09-MAY-2000.
 XX

PF 24-JUL-1998; 98US-00122443.
 XX
 PR 25-JUL-1997; 97US-0053765P.
 XX (SCHE) SCHERING CORP.
 PA Bazan JF;
 PI
 XX
 DR WPI: 2000-364420/31.
 DR N-PSDB; AAA52577.
 XX
 PT Novel recombinant DNA encoding cytokines especially interleukin-B30
 PT useful as probes or primers for diagnosing immune disorders including
 PT autoimmune or chronic inflammatory conditions.
 XX
 PS Claim 1; Col 5-8; 32pp; English.
 XX
 CC This sequence represents human interleukin-B30 (IL-B30). IL-B30 is a
 CC novel cytokine, exhibiting significant homology to IL-6 and GCSF
 CC (granulocyte colony stimulating factor). Cytokines play a critical role
 CC in signalling between immune or other cells during an immune response.
 CC The precise role of IL-B30 is not yet known - it is likely to have either
 CC a stimulatory or an inhibitory effect on haematopoietic cells such as T-
 CC cells, B-cells, natural killer (NK) cells and macrophages. Alternatively,
 CC it may affect vascular physiology or development, or have neuronal
 CC effects. IL-B30, its fragments, IL-B30 nucleotides, agonists and
 CC antagonists are useful in the diagnosis and treatment of disorders
 CC associated with abnormal expression or activity of IL-B30 e.g.,
 CC inflammatory or autoimmune disorders. Nucleotides encoding IL-B30 are
 CC useful for recombinant expression of IL-B30 in a host cell, and as a
 CC source of probes and primers. The IL-B30 probes and primers can be used
 CC to detect levels of IL-B30 expression in samples from patients suspected
 CC of having an inflammatory or autoimmune disorder. IL-B30 nucleotides may
 CC also be used to identify homologous genes in other species. IL-B30
 CC protein or its fragments are useful as antigens for raising antibodies to
 CC various linear and conformational epitopes. Such antibodies may be used
 CC to detect levels of IL-B30 protein in a sample
 XX
 SQ Sequence 189 AA;

Query Match 100.0%; Score 1004; DB 3; Length 189;
 Best Local Similarity 100.0%; Pred. No. 6.2e-97;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGSRVAVMLLLPWTAGRAVPGSSPAWTCQQLSQKLCCTLAWSAHLVGHMDLREG 60
 DB 1 MLGSRVAVMLLLPWTAGRAVPGSSPAWTCQQLSQKLCCTLAWSAHLVGHMDLREG 60
 QY 61 DEETNDVPHIQCGDQDQGLRDNQFCLQRIHQGLIFYEKLGSDFITGSPSLPDPSP 120
 DB 61 DEETNDVPHIQCGDQDQGLRDNQFCLQRIHQGLIFYEKLGSDFITGSPSLPDPSP 120
 QY 121 VAQLHASLGLSQLQPEGHWHETQIQPSLSPSQWRLRLFRKILRSIQAFVAVARVF 180
 DB 121 VAQLHASLGLSQLQPEGHWHETQIQPSLSPSQWRLRLFRKILRSIQAFVAVARVF 180
 QY 181 AHGAATLSP 189
 DB 181 AHGAATLSP 189

RESULT 4

AAB47120
 ID AAB47120 standard; protein; 189 AA.
 XX
 AC AAB47120;
 XX
 DT 04-JUN-2001 (first entry)
 XX
 DE Human IL-B30.
 XX
 KW Human; mouse; interleukin-B30; IL-12 p40; IL-B30; interferon-gamma;
 KW IFNgamma; Th1 response; autoimmune disease; chronic inflammation;

KW memory T-cell; leukocyte; rheumatoid arthritis; osteoarthritis;
 KW atherosclerosis; multiple sclerosis; vasculitis; spinal injury;
 KW delayed hypersensitivity; skin graft; transplant; cancer; stroke;
 KW neurodegeneration; ischaemia; postmenopausal osteoporosis;
 KW Castleman's disease.
 XX
 OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..21
 FT /note= "Signal peptide"
 FT Protein 22..189
 FT /note= "Mature protein"
 XX
 XX WO200118051-A2.
 XX
 PD 15-MAR-2001.
 XX
 XX 08-SEP-2000; 2000WO-US024686.
 PF
 XX
 PR 09-SEP-1999; 99US-00393090.
 PR 10-NOV-1999; 99US-0164616P.
 XX
 XX (SCHE) SCHERING CORP.
 XX
 PI Opmann B, De Waal Malefyt R, Rennick DM, Kastelein RA;
 PI Wiekowski MT, Lira SA, Narula SK;
 XX
 DR WPI: 2001-244560/25.
 DR N-PSDB; AAC85540.
 XX
 CC Composition comprising interleukin-12 p40 and IL-B30 polypeptide or its
 CC segment, useful for ameliorating rheumatoid arthritis, osteoarthritis,
 CC atherosclerosis, multiple sclerosis, vasculitis and tumor.
 XX
 PS Disclosure; Page 10-11; 69pp; English.
 XX
 CC This sequence shows human interleukin-B30. Fragments of this protein may
 CC be used in the composition of the invention. The composition comprises a
 CC substantially pure polypeptide comprising a number of distinct segments
 CC of at least 7 contiguous amino acids from IL-12 p40 and/or IL-B30, and a
 CC substantially pure polypeptide comprising a segment of at least 11
 CC contiguous amino acids from IL-12 p40 and/or IL-B30. The composition is
 CC useful for modulating physiology or development of a cell or tissue in a
 CC host organism, resulting in an increased or decreased production of
 CC interferon-gamma (IFNgamma), an enhanced Th1 response such as anti-tumor
 CC effect, adjuvant effect, anti-viral effect or antagonized allergic
 CC effect, and amelioration of an autoimmune condition or a chronic
 CC inflammatory condition. IL-B30 or its agonist is useful inducing the
 CC proliferation of memory T-cells. An agonist or antagonist of IL-B30
 CC protein is useful for modulating the trafficking or activation of a
 CC leukocyte in an animal experiencing science or symptoms of autoimmunity,
 CC an inflammatory condition, tissue specific autoimmunity, degenerative
 CC autoimmunity, rheumatoid arthritis, osteoarthritis, atherosclerosis,
 CC multiple sclerosis, vasculitis, delayed hypersensitivities, skin
 CC grafting, a transplant, spinal injury, stroke, neurodegeneration, an
 CC infectious disease, ischaemia, cancer, tumor, multiple myeloma,
 CC Castleman's disease, postmenopausal osteoporosis or IL-6-associated
 CC diseases. IL-12 p40/IL-B30 is useful as an immunogen for the production a
 CC antisera or antibodies specific for binding
 XX
 SQ Sequence 189 AA;

Query Match 100.0%; Score 1004; DB 4; Length 189;
 Best Local Similarity 100.0%; Pred. No. 6.2e-97;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGSRVAVMLLLPWTAGRAVPGSSPAWTCQQLSQKLCCTLAWSAHLVGHMDLREG 60
 DB 1 MLGSRVAVMLLLPWTAGRAVPGSSPAWTCQQLSQKLCCTLAWSAHLVGHMDLREG 60
 QY 61 DEETNDVPHIQCGDQDQGLRDNQFCLQRIHQGLIFYEKLGSDFITGSPSLPDPSP 120

Db 61 DEETTNDVPHIQCGDGDPOGLRDNSQFCLQRIHQGLIFYEKLKLSGDI FTGEPSSLDPSP 120
 Qy 121 VAQLHASLLGLSQQLOPEGHWHWTQQIPSPSPQWQRLRLFKILRSLOAFVAAARVF 180
 Db 121 VAQLHASLLGLSQQLOPEGHWHWTQQIPSPSPQWQRLRLFKILRSLOAFVAAARVF 180
 Qy 181 AHGAATLSP 189
 Db 181 AHGAATLSP 189
 RESULT 5
 ID ABU08268 standard; protein; 189 AA.
 AC ABU08268;
 XX
 DT 19-MAY-2003 (first entry)
 DE Human interleukin-B30, IL-B30.
 XX
 KW Human; interleukin-B30; IL-B30; inflammation; lymphoid cell;
 KW immunosuppressive; autoimmune disorder; immunomodulatory;
 KW anti-inflammatory; vascular; neuroprotective; immunological response;
 KW haematopoietic cell disorder; vascular physiology; development.
 XX
 OS Homo sapiens.
 XX
 XX
 PH Key Location/Qualifiers
 FT Peptide 1..21
 FT /label= Signal_peptide
 FT Protein 22..189
 FT /label= Mature IL B30
 FT /note= "This protein is specifically claimed in claim 3"
 XX
 PN US6495667-B1.
 XX
 PD 17-DEC-2002.
 XX
 XX 25-APR-2000; 2000US-00558087.
 XX
 XX 25-JUL-1997; 97US-0053765P.
 PR 24-JUL-1998; 98US-00122443.
 XX
 XX (SCHE) SCHERING CORP.
 XX
 XX Bazan JF;
 XX
 XX WPI; 2003-327470/31.
 DR N-PSDB; ABX13358.
 XX
 XX Binding compounds comprising antibodies which bind to Interleukin B30,
 PT useful for treating disorders associated with hematopoietic cells, e.g.
 PT inflammation and autoimmune diseases and development disorders.
 XX
 XX Claim 1; Col 5-6; 31pp; English.
 PS
 XX The invention relates to a binding compound comprising an antibody
 CC binding site which specifically binds to residues 1-168 (mature human
 CC interleukin-B30, IL-B30). Also included is a method of making the binding
 CC composition, comprising administering to an animal: (a) a substantially
 CC pure and isolated polypeptide comprising residues 1-168 of mature human
 CC IL-B30; (b) a substantially pure and isolated polypeptide comprising
 CC residues 1-175 of a mouse IL-B30; and/or (c) a substantially pure or
 CC isolated polypeptide comprising pig mature IL-B30. The animal produces
 CC the binding compound. The binding compound may be administered to treat
 CC disorders associated with haematopoietic cells, e.g., lymphoid cells,
 CC which affect immunological responses, e.g., inflammation and/or
 CC autoimmune disorders. Alternatively, it may affect vascular physiology or
 CC development, or neuronal effects. The present sequence represents full-
 CC length human IL-B30
 XX
 SQ Sequence 189 AA;

Query Match 100.0%; Score 1004; DB 6; Length 189;
 Best Local Similarity 100.0%; Pred. No. 6.2e-97;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MLGSRVAMLLLLPWTQAQRAVPGGSSPAWTCQQLSQKLTCLAWSAHPLVGHMDLREEG 60
 Db 1 MLGSRVAMLLLLPWTQAQRAVPGGSSPAWTCQQLSQKLTCLAWSAHPLVGHMDLREEG 60
 Qy 61 DEETTNDVPHIQCGDGDPOGLRDNSQFCLQRIHQGLIFYEKLKLSGDI FTGEPSSLDPSP 120
 Db 61 DEETTNDVPHIQCGDGDPOGLRDNSQFCLQRIHQGLIFYEKLKLSGDI FTGEPSSLDPSP 120
 Qy 121 VAQLHASLLGLSQQLOPEGHWHWTQQIPSPSPQWQRLRLFKILRSLOAFVAAARVF 180
 Db 121 VAQLHASLLGLSQQLOPEGHWHWTQQIPSPSPQWQRLRLFKILRSLOAFVAAARVF 180
 Qy 181 AHGAATLSP 189
 Db 181 AHGAATLSP 189
 RESULT 6
 ID ABG75811 standard; protein; 189 AA.
 XX
 AC ABG75811;
 XX
 DT 09-MAY-2003 (first entry)
 DE Human interleukin-B30 (IL-B30).
 XX
 KW Human; antigenic; cytokine; interleukin-B30; IL-B30; protein therapy;
 KW inflammatory condition; autoimmune disorder; activation; development;
 KW differentiation; function; haematopoietic cell; lymphoid cell; immunogen;
 KW antiinflammatory; immunosuppressive.
 XX
 OS Homo sapiens.
 XX
 XX
 PH Key Location/Qualifiers
 FT Peptide 1..21
 FT /label= Signal_peptide
 FT Protein 22..189
 FT /label= Mature_IL-B30_protein
 XX
 XX US6479634-B1.
 XX
 XX 12-NOV-2002.
 XX
 XX 25-APR-2000; 2000US-00558089.
 XX
 XX 25-JUL-1997; 97US-0053765P.
 PR 24-JUL-1998; 98US-00122443.
 XX
 XX (SCHE) SCHERING CORP.
 XX
 XX Bazan JF;
 XX
 XX WPI; 2003-298116/29.
 DR N-PSDB; ABX11988.
 XX
 XX New interleukin-B30 (IL-B30) polypeptide, useful for diagnosing or
 PT treating e.g. inflammatory conditions or autoimmune disorders, or in
 PT regulating the development of hematopoietic cells or lymphoid cells.
 XX
 XX Claim 2; Col 5-8; 31pp; English.
 PS
 XX The invention discloses an isolated antigenic mature polypeptide that is
 CC a mammalian cytokine designated interleukin-B30 (IL-B30). The IL-B30
 CC polypeptide is useful for diagnosing or treating (e.g. protein therapy)
 CC conditions associated with abnormal physiology or development (e.g.
 CC inflammatory conditions or autoimmune disorders), or in regulating the
 CC activation, development, differentiation and function of haematopoietic

CC cells or lymphoid cells. The IL-B30 polypeptide is also useful as an
 CC immunogen for producing antisera or antibodies specific for binding. The
 CC sequence presented is the human IL-B30 protein
 XX
 SQ Sequence 189 AA;

Query Match 100.0%; Score 1004; DB 6; Length 189;
 Best Local Similarity 100.0%; Pred. No. 6.2e-97;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGSRVAVMLLLPWTAGRAVPGSSPAWTCQQLSQKLTAWSAHPLVGHMDLREEG 60
 Db 1 MLGSRVAVMLLLPWTAGRAVPGSSPAWTCQQLSQKLTAWSAHPLVGHMDLREEG 60
 QY 61 DEETNDVPHICGDCDPOGLRDNQFCQRIHQGLIFYEKLGSDIFTGEPSSLPS 120
 Db 61 DEETNDVPHICGDCDPOGLRDNQFCQRIHQGLIFYEKLGSDIFTGEPSSLPS 120
 QY 121 VAQLHASLLGLSQQLQPEGHWHWETQIPSLSPSQPWQRLRLFKILRSLOAFVAVARVF 180
 Db 121 VAQLHASLLGLSQQLQPEGHWHWETQIPSLSPSQPWQRLRLFKILRSLOAFVAVARVF 180
 QY 181 AHGAATLSP 189
 Db 181 AHGAATLSP 189

RESULT 7
 ADF70612
 ID ADF70612 standard; protein; 189 AA.
 AC ADF70612;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human interleukin B30.
 XX
 KW Human; interleukin B30; IL-B30; IL-12 p40; tumour necrosis factor alpha;
 KW IFN-alpha; interferon alpha; chronic inflammatory condition;
 KW memory T-cell; tumour; anti-viral; vaccine; allergic responses;
 KW autoimmune disease; multiple sclerosis; rheumatoid arthritis;
 KW inflammatory bowel disease; psoriasis.
 XX
 OS Homo sapiens.
 XX
 FN US2003162261-A1.
 XX
 PD 28-AUG-2003.
 XX
 PF 27-FEB-2003; 2003US-00375706.
 XX
 PR 09-SEP-1999; 99US-0153281P.
 PR 10-NOV-1999; 99US-0164616P.
 PR 08-SEP-2000; 2000US-00658699.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 PI Oppmann B, De Waal Malefyt R, Rennick DM, Kastelein RA;
 PI Wiekowski MT, Lira SA, Narula SK;
 XX
 DR WPI; 2003-897932/82.
 DR N-PSDB; ADF70611.
 XX
 PT Composition comprising fragments from interleukin (IL)-12 p40 and IL-B30
 PT polypeptides is useful to enhance anti-viral, anti-tumour and vaccine
 PT effects and to antagonize allergic responses.
 XX
 PS Example 2; SEQ ID NO 2; 34pp; English.
 XX
 CC The invention relates to a composition comprising polypeptide fragments
 CC from interleukin (IL)-12 p40 and IL-B30 is new. The fragments comprise 7
 CC or 11 contiguous amino acids. Also included are an isolated or
 CC recombinant nucleic acid (NI) encoding the polypeptides of the novel

CC composition, a cell comprising recombinant N1, a nucleic acid which
 CC hybridises the natural coding portion of primate IL-12 p40 and primate IL
 CC -30, an antagonist of IL-12 p40/IL-B30 (combined with a tumour necrosis
 CC factor (TNF) alpha antagonist, an IL-12 antagonist, IL-10 or steroids), a
 CC binding compound comprising an antigen binding site from an antibody
 CC which specifically binds to the novel composition, producing an
 CC antigen-antibody complex, modulating physiology or development of a cell
 CC or tissue comprising contacting the cell with the claimed composition to
 CC increase production of IFN-alpha, modulating physiology or development of
 CC a cell in a host organism (comprising administering the novel composition
 CC which results in an anti-tumour, adjuvant, anti-viral or antagonised
 CC allergic effect), administering the IL-12 p40/IL-B30 antagonist resulting
 CC in amelioration of an autoimmune condition or a chronic inflammatory
 CC condition, increasing secretion of a primate IL-B30 (comprising
 CC expressing IL-B30 with IL-12 p40 or increasing secretion of IL-12 p40
 CC comprising expressing IL-12 p40 with IL-B30), screening for a receptor
 CC which binds the novel composition, modulating the inflammatory response
 CC in an animal and inducing the proliferation of memory T-cells by
 CC administering IL-B30 or its agonist. The invention is useful in
 CC forensics, research and teaching. They are useful to treat conditions
 CC associated with abnormal physiology including inflammatory conditions.
 CC particularly the complex is useful to enhance anti-tumour, anti-viral and
 CC vaccine responses and to antagonise allergic responses. Antagonists may
 CC be useful to treat autoimmune diseases such as multiple sclerosis or
 CC psoriasis or chronic inflammatory conditions such as rheumatoid arthritis
 CC or inflammatory bowel disease. The present sequence represents human IL-
 CC B30.
 XX
 SQ Sequence 189 AA;

Query Match 100.0%; Score 1004; DB 7; Length 189;
 Best Local Similarity 100.0%; Pred. No. 6.2e-97;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGSRVAVMLLLPWTAGRAVPGSSPAWTCQQLSQKLTAWSAHPLVGHMDLREEG 60
 Db 1 MLGSRVAVMLLLPWTAGRAVPGSSPAWTCQQLSQKLTAWSAHPLVGHMDLREEG 60
 QY 61 DEETNDVPHICGDCDPOGLRDNQFCQRIHQGLIFYEKLGSDIFTGEPSSLPS 120
 Db 61 DEETNDVPHICGDCDPOGLRDNQFCQRIHQGLIFYEKLGSDIFTGEPSSLPS 120
 QY 121 VAQLHASLLGLSQQLQPEGHWHWETQIPSLSPSQPWQRLRLFKILRSLOAFVAVARVF 180
 Db 121 VAQLHASLLGLSQQLQPEGHWHWETQIPSLSPSQPWQRLRLFKILRSLOAFVAVARVF 180
 QY 181 AHGAATLSP 189
 Db 181 AHGAATLSP 189

RESULT 8
 ADQ14469
 ID ADQ14469 standard; protein; 189 AA.
 XX
 AC ADQ14469;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Human interleukin-19 protein.
 XX
 KW Wound healing; agonist; antagonist; interleukin-23; IL-23; vulnerary;
 KW cytokine; human; interleukin-19; IL-19.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT Peptide 1..21
 FT Protein /note= "Signal peptide"
 FT Protein /note= "Mature protein"
 XX
 PN WO2004058178-A2.

XX	PD	15-JUL-2004.	Peptide	1. .21	
XX	PF	18-DEC-2003; 2003WO-US040937.	Protein	/note= "Signal peptide"	
XX	PR	23-DEC-2002; 2002US-0436274P.		22. .189	
XX	PA	(SCHE) SCHERING CORP.		/note= "Mature IL-23p19"	
XX	PI	Bowman BP, Chen S, Cua DJ;			
XX	DR	WPI; 2004-525781/50.			
XX	DR	N-PSDB; ADQ14468.			
XX	PT	Treating inflammatory skin disorders or improving wound healing comprises administering to a subject an agonist or antagonist of interleukin-23.			
XX	PS	Example; SEQ ID NO 4; 52pp; English.			
XX	CC	The invention relates to a novel method for treating or improving wound healing. The method comprises administering to a subject an agonist or antagonist of interleukin (IL)-23. The invention further comprises: an agonist of IL-23 derived from the binding site of an antibody that specifically binds to an IL-23 receptor; and a kit comprising the agonist and a compartment or instructions for use or disposal. The interleukin-23 agents have vulnerary activity. The method is useful for treating or improving wound healing. This sequence represents a cytokine human interleukin-19 protein used in the wound healing method of the invention.			
XX	SEQ	Sequence 189 AA;			
Query Match 100.0%; Score 1004; DB 8; Length 189;					
Best Local Similarity 100.0%; Pred. No. 6.2e-97;					
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Db	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Qy	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Db	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Qy	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Db	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Qy	181	AHGAATLSP 189			
Db	181	AHGAATLSP 189			
Query Match 100.0%; Score 1004; DB 8; Length 189;					
Best Local Similarity 100.0%; Pred. No. 6.2e-97;					
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Db	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Qy	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Db	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Qy	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Db	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Qy	181	AHGAATLSP 189			
Db	181	AHGAATLSP 189			
Query Match 100.0%; Score 1004; DB 8; Length 189;					
Best Local Similarity 100.0%; Pred. No. 6.2e-97;					
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Db	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Qy	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Db	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Qy	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Db	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Qy	181	AHGAATLSP 189			
Db	181	AHGAATLSP 189			
Query Match 100.0%; Score 1004; DB 8; Length 189;					
Best Local Similarity 100.0%; Pred. No. 6.2e-97;					
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Db	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Qy	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Db	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Qy	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Db	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Qy	181	AHGAATLSP 189			
Db	181	AHGAATLSP 189			
Query Match 100.0%; Score 1004; DB 8; Length 189;					
Best Local Similarity 100.0%; Pred. No. 6.2e-97;					
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Db	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Qy	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Db	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Qy	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Db	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Qy	181	AHGAATLSP 189			
Db	181	AHGAATLSP 189			
Query Match 100.0%; Score 1004; DB 8; Length 189;					
Best Local Similarity 100.0%; Pred. No. 6.2e-97;					
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Db	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Qy	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Db	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Qy	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Db	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Qy	181	AHGAATLSP 189			
Db	181	AHGAATLSP 189			
Query Match 100.0%; Score 1004; DB 8; Length 189;					
Best Local Similarity 100.0%; Pred. No. 6.2e-97;					
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Db	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Qy	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Db	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Qy	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Db	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Qy	181	AHGAATLSP 189			
Db	181	AHGAATLSP 189			
Query Match 100.0%; Score 1004; DB 8; Length 189;					
Best Local Similarity 100.0%; Pred. No. 6.2e-97;					
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Db	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Qy	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Db	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Qy	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Db	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Qy	181	AHGAATLSP 189			
Db	181	AHGAATLSP 189			
Query Match 100.0%; Score 1004; DB 8; Length 189;					
Best Local Similarity 100.0%; Pred. No. 6.2e-97;					
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Db	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Qy	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Db	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Qy	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Db	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Qy	181	AHGAATLSP 189			
Db	181	AHGAATLSP 189			
Query Match 100.0%; Score 1004; DB 8; Length 189;					
Best Local Similarity 100.0%; Pred. No. 6.2e-97;					
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Db	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Qy	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Db	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Qy	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Db	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Qy	181	AHGAATLSP 189			
Db	181	AHGAATLSP 189			
Query Match 100.0%; Score 1004; DB 8; Length 189;					
Best Local Similarity 100.0%; Pred. No. 6.2e-97;					
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Db	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Qy	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Db	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Qy	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Db	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Qy	181	AHGAATLSP 189			
Db	181	AHGAATLSP 189			
Query Match 100.0%; Score 1004; DB 8; Length 189;					
Best Local Similarity 100.0%; Pred. No. 6.2e-97;					
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Db	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Qy	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Db	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Qy	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Db	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Qy	181	AHGAATLSP 189			
Db	181	AHGAATLSP 189			
Query Match 100.0%; Score 1004; DB 8; Length 189;					
Best Local Similarity 100.0%; Pred. No. 6.2e-97;					
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Db	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Qy	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Db	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Qy	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Db	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Qy	181	AHGAATLSP 189			
Db	181	AHGAATLSP 189			
Query Match 100.0%; Score 1004; DB 8; Length 189;					
Best Local Similarity 100.0%; Pred. No. 6.2e-97;					
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Db	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Qy	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Db	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Qy	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Db	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Qy	181	AHGAATLSP 189			
Db	181	AHGAATLSP 189			
Query Match 100.0%; Score 1004; DB 8; Length 189;					
Best Local Similarity 100.0%; Pred. No. 6.2e-97;					
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Db	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Qy	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Db	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Qy	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Db	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Qy	181	AHGAATLSP 189			
Db	181	AHGAATLSP 189			
Query Match 100.0%; Score 1004; DB 8; Length 189;					
Best Local Similarity 100.0%; Pred. No. 6.2e-97;					
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Db	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Qy	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Db	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Qy	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Db	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Qy	181	AHGAATLSP 189			
Db	181	AHGAATLSP 189			
Query Match 100.0%; Score 1004; DB 8; Length 189;					
Best Local Similarity 100.0%; Pred. No. 6.2e-97;					
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Db	1	MLGSRAVM L L L L L P W T A Q G R A V P G S S P A W T C Q Q L S Q K L T C L A W S A P L V G H M D L R E E G 60			
Qy	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Db	61	DEETTNDVPHIQCGDGDPOGLRDNQFCQLRIHQGLIFYEKLGSDIFTGEPSSLDPSP 120			
Qy	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Db	121	VAQLHASLLGLSLLQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFLKILRSLOAFVAAARVF 180			
Qy	181	AHGAATLSP 189			
Db	181	AHGAATLSP 189			

XX ADV98151;
 XX 10-MAR-2005 (first entry)
 XX Novel human interleukin B30 protein.
 XX DNA purification; cytokine; interleukin-B30; IL-B30; inflammation;
 KW autoimmune disorder; forensic science; differential expression.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH Peptide 1..21
 FT /note= "signal peptide"
 FT Protein 22..189
 FT /note= "mature IL-B30 protein"
 XX
 XX US6835825-B1.
 XX 28-DEC-2004.
 XX 25-APR-2000; 2000US-00558474.
 XX 25-JUL-1997; 97US-0053765P.
 PR 24-JUL-1998; 98US-00122443.
 XX (SCHE) SCHERING CORP.
 XX Bazan JF;
 XX WPI; 2005-077885/09.
 DR N-PSDB; ADV98150, ADV98152.
 XX
 XX Detecting interleukin-B30 polynucleotide, comprises contacting
 PT polynucleotide with probe capable of hybridizing with contiguous
 PT nucleotides of polynucleotide to form duplex, where detection of duplex
 PT indicates presence of polynucleotide.
 XX
 XX Disclosure; SEQ ID NO 2; 32pp; English.
 XX
 XX The invention relates to a method of detecting (M1) a polynucleotide, by
 CC contacting a polynucleotide with a probe (PB) that hybridizes, under
 CC stringent wash conditions to at least 394 or 25 contiguous nucleotides of
 CC open reading frame of a fully defined interleukin (IL)-B30 sequence of
 CC 570 (S1) or 1203 (S2) base pairs, to form duplex, where detection of
 CC duplex indicates presence of polynucleotide. The method is useful for
 CC detecting IL-B30 polynucleotide. The method is useful for detecting the
 CC expression of IL-B30 polynucleotide, and for detecting levels of IL-B30
 CC in samples from patient suspected of having abnormal conditions such as
 CC inflammatory or autoimmune. The method is also useful in forensic
 CC science, e.g. to distinguish rodent from human or to distinguish between
 CC different cell exhibiting differential expression or modification
 CC patterns. The method is further useful for detecting disease or disorder
 CC associated with abnormal expression or signaling by IL-B30. This sequence
 CC corresponds to the novel interleukin-B30 protein.
 XX
 XX Sequence 189 AA;
 SQ
 Query Match 100.0%; Score 1004; DB 9; Length 189;
 Best Local Similarity 100.0%; Pred. No. 6.2e-97;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGSAVAMLLLLPMTAQGRAVPGSSPAWTCQQLSQKLCCTLAWSAHPVGHMDLREEG 60
 DB 1 MLGSAVAMLLLLPMTAQGRAVPGSSPAWTCQQLSQKLCCTLAWSAHPVGHMDLREEG 60
 QY 61 DEETNDVPHICGCGDQPGRLDMSQFCLORIHQGLIFYEKLGSDFITGSPSLPDS 120
 DB 61 DEETNDVPHICGCGDQPGRLDMSQFCLORIHQGLIFYEKLGSDFITGSPSLPDS 120
 QY 121 VAQLHASLLGLSQLQPEGHWHWTQOIPSLSPSQPWQRLRLFRKILRSIQAFVAVARVF 180
 DB 121 VAQLHASLLGLSQLQPEGHWHWTQOIPSLSPSQPWQRLRLFRKILRSIQAFVAVARVF 180

DB 121 VAQLHASLLGLSQLQPEGHWHWTQOIPSLSPSQPWQRLRLFRKILRSIQAFVAVARVF 180
 QY 181 AHGAATLSP 189
 DB 181 AHGAATLSP 189
 RESULT 11
 AEA51094
 ID AEA51094 standard; protein; 189 AA.
 XX
 XX AEA51094;
 XX 11-AUG-2005 (first entry)
 XX Human p19 protein.
 XX
 KW Diagnosis; therapeutic; asthma; antiasthmatic; immune disorder;
 KW inflammation; respiratory disease; allergy; anti-allergic;
 KW chronic obstructive pulmonary disease; respiratory-gen.;
 KW pulmonary fibrosis; antiinflammatory; pneumonia; infection; p19 protein.
 XX Homo sapiens.
 XX WO2005052157-A1.
 XX 09-JUN-2005.
 XX 18-NOV-2004; 2004WO-US038886.
 PR 21-NOV-2003; 2003US-00720026.
 XX (SCHE) SCHERING CORP.
 XX Chirica M, Kastelein RA, Moore KW, Parham CL;
 DR WPI; 2005-418000/42.
 DR N-PSDB; AEA51093.
 XX
 PT Use of an agonist or antagonist of DNAX cytokine receptor subunit 5
 PT (DCRS5) or of p19 for treating a human subject experiencing a
 PT physiological disorder such as allergy or chronic obstructive pulmonary
 disorder (COPD).
 XX
 XX Claim 1; SEQ ID NO 6; 89pp; English.
 CC The present invention relates to a method of treating a human subject
 CC experiencing a physiological disorder. The method involves administering
 CC an agonist or antagonist of DNAX cytokine receptor subunit 5 (DCRS5), also
 CC known as IL-23R) or of p19, where the disorder comprises asthma or
 CC allergy, chronic obstructive pulmonary disorder (COPD) or an interstitial
 CC lung disorder. The invention is useful for treating interstitial lung
 CC disorder e.g. idiopathic pulmonary fibrosis, eosinophilic granuloma and
 CC hypersensitivity pneumonitis. The present sequence is the human p19
 CC protein.
 XX
 XX Sequence 189 AA;
 SQ
 Query Match 100.0%; Score 1004; DB 9; Length 189;
 Best Local Similarity 100.0%; Pred. No. 6.2e-97;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGSAVAMLLLLPMTAQGRAVPGSSPAWTCQQLSQKLCCTLAWSAHPVGHMDLREEG 60
 DB 1 MLGSAVAMLLLLPMTAQGRAVPGSSPAWTCQQLSQKLCCTLAWSAHPVGHMDLREEG 60
 QY 61 DEETNDVPHICGCGDQPGRLDMSQFCLORIHQGLIFYEKLGSDFITGSPSLPDS 120
 DB 61 DEETNDVPHICGCGDQPGRLDMSQFCLORIHQGLIFYEKLGSDFITGSPSLPDS 120
 QY 121 VAQLHASLLGLSQLQPEGHWHWTQOIPSLSPSQPWQRLRLFRKILRSIQAFVAVARVF 180
 DB 121 VAQLHASLLGLSQLQPEGHWHWTQOIPSLSPSQPWQRLRLFRKILRSIQAFVAVARVF 180

```
QY      181 AHGAATLSP 189
      |||||
Db      181 AHGAATLSP 189
      |||||

RESULT 12
AEB47331
XX      AEB47331 standard; protein; 189 AA.
AC      AEB47331;
XX
XX      22-SEP-2005 (first entry)
XX
XX      Human interleukin-B30 (IL-B30) protein, SEQ ID NO: 2.
XX
XX      IL; interleukin; cell differentiation; diagnostic; gene therapy;
XX      drug screening; inflammation; antiinflammatory.
XX
XX      Homo sapiens.
XX
XX      Key      Location/Qualifiers
XX      Peptide  1..21
XX      /label= Signal_peptide
XX      Protein  22..189
XX      /note= "Mature human interleukin-30 (IL-B30) protein"
XX
XX      US2005158750-A1.
XX
XX      21-JUL-2005.
XX
XX      06-DEC-2004; 2004US-00006154.
XX
XX      25-APR-2000; 2000US-00558474.
XX
XX      (SCHE ) SCHERING CORP.
XX
XX      Bazan JF;
XX
XX      WPI; 2005-512254/52.
XX      N-PSDB; AEB47330.
XX
XX      New isolated or recombinant polynucleotide encoding an antigenic
XX      interleukin-B30 (IL-B30), useful in diagnostic applications for IL-B30
XX      mediated conditions such as inflammatory conditions.
XX
XX      Claim 1; SEQ ID NO 2; 35pp; English.
XX
XX      The present invention relates to recombinant polynucleotide encoding an
XX      antigenic interleukin-B30 (IL-B30). The polynucleotides are useful for
XX      detecting, isolating, or identifying a DNA clone encoding IL-B30 e.g.
XX      from a natural source, particularly for isolating a gene from mammal. The
XX      proteins are useful for generating antibodies and for screening drugs.
XX      The invention is also useful for diagnostic applications for IL-B30
XX      mediated conditions such as inflammatory conditions and for cell
XX      differentiation. The invention is also useful in gene therapy. The
XX      present sequence is the human ILB-30 protein.
XX
XX      Sequence 189 AA;

Query Match      100.0%; Score 1004; DB 9; Length 189;
Best Local Similarity 100.0%; Pred. No. 6.2e-97;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLGSRVWMLLLLPWTAQGRVPGSSPAWTCQOQLSQKLTCLAWSAHPLVGHMDLREEG 60
      |||||
Db      1 MLGSRVWMLLLLPWTAQGRVPGSSPAWTCQOQLSQKLTCLAWSAHPLVGHMDLREEG 60
      |||||

QY      61 DEETTNDVPHIQCGDGPQGLRDNQFCQLQRIHQGLIFYEKLGSDFITGEPSSLDPSP 120
      |||||
Db      61 DEETTNDVPHIQCGDGPQGLRDNQFCQLQRIHQGLIFYEKLGSDFITGEPSSLDPSP 120
      |||||

QY      121 VAQLHASLLGLSLLQPEGHWHWTQQTSPSLSPSQPWQRLRLRFLKILRSLOAFVAARVF 180
      |||||
Db      121 VAQLHASLLGLSLLQPEGHWHWTQQTSPSLSPSQPWQRLRLRFLKILRSLOAFVAARVF 180
      |||||

RESULT 13
AAY94966
ID      AAY94966 standard; protein; 189 AA.
XX
XX      AAY94966;
XX
XX      16-JUN-2000 (first entry)
XX
XX      Human secreted protein clone rk80_3 protein sequence SEQ ID NO:138.
XX
XX      Human; secreted protein; immunestimulant; immunosuppressant; virucide;
XX      antibacterial; antifungal; cytostatic; antiinflammatory; dermatological;
XX      antidiabetic; antiasthmatic; antiarthritic; antirheumatic; protozoacide;
XX      antithyroid; immune deficiency; severe combined immunodeficiency; SCID;
XX      infection; HIV; hepatitis; malaria; autoimmune disorder; systemic lupus;
XX      connective tissue disease; multiple sclerosis; erythematosis;
XX      rheumatoid arthritis; autoimmune pulmonary inflammation; asthma;
XX      Guillain-Barre syndrome; autoimmune thyroiditis; myasthenia Gravis;
XX      insulin dependent diabetes mellitus; graft-versus-host-disease;
XX      autoimmune inflammatory eye disease; allergy.
XX
XX      Homo sapiens.
XX
XX      WO200009552-A1.
XX
XX      24-FEB-2000.
XX
XX      13-AUG-1999; 99WO-US018298.
XX
XX      14-AUG-1998; 98US-0096622P.
XX      17-AUG-1998; 98US-0096815P.
XX      04-SEP-1998; 98US-0099229P.
XX      23-OCT-1998; 98US-0105368P.
XX      08-JAN-1999; 99US-0115234P.
XX      12-FEB-1999; 99US-0119331P.
XX      18-FEB-1999; 99US-0120575P.
XX      30-APR-1999; 99US-0132020P.
XX      11-AUG-1999; 99US-0148424P.
XX
XX      (GEMY ) GENETICS INST INC.
XX
XX      Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans Ci,
XX      Merberg D, Treacy M, Agostino MJ, Steininger RJ, Spaulding V;
XX      Wong GG, Clark HF, Fectel K;
XX
XX      WPI; 2000-205979/18.
XX
XX      New polynucleotides encoding secreted proteins, which may have e.g.
XX      nutritional, chemokine, immune stimulating or suppressing, hematopoiesis
XX      regulating, tissue growth, activin/inhibin antiinflammatory or tumor
XX      inhibition activity.
XX
XX      Claim 147; Page 597; 641pp; English.
XX
XX      AAA16618 to AAA16697 encode the human secreted proteins given in AAY94898
XX      to AAY94980, isolated from human adult brain, adult thyroid, adult
XX      retina, foetal carcinoma, adult blood, adult neural, foetal kidney, adult
XX      placenta, adult testis, whole embryo, adult cartilage, kidney, foetal
XX      brain, adult thymus, foetal placenta, adult uterus, adult tumour, and
XX      adult bladder, cDNA libraries. The polynucleotides and proteins are
XX      predicted to have biological activities which would make them suitable
XX      for treating, preventing or ameliorating medical conditions in humans and
XX      animals. The polynucleotides can be used as markers for tissues in which
XX      the protein is preferentially expressed, as molecular weight markers on
XX      Southern gels, and as chromosome markers or tags to identify chromosomes
```

or to map gene positions. The proteins can be used in the treatment of immune deficiencies and disorders, such as severe combined immunodeficiency (SCID), as well as viral, bacterial, fungal and other infections. These infections include human immunodeficiency virus (HIV), hepatitis, herpesviruses, mycobacteria, leishmania spp., malaria and candidiasis. The proteins can be used to treat autoimmune disorders such as connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host-disease and autoimmune inflammatory eye disease. The proteins can also be used to treat allergic conditions, such as asthma. AAA16698 to AAA16774 represent probes for the human secreted proteins from the present invention

XX Sequence 189 AA;

Query Match 99.6%; Score 1000; DB 3; Length 189;
Best Local Similarity 99.5%; Pred. No. 1.6e-96;
Matches 188; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSRVAVMLLLPWTAGRAVPGSSPAWTCQQLSQKLTLSAHPVGHMDLREEG 60
DB 1 MGSRVAVMLLLPWTAGRAVPGSSPAWTCQQLSQKLTLSAHPVGHMDLREEG 60

QY 61 DEETNDVPHIQCGDQDPOGLRDNQFCLQRIHQGLIFYEKLGLSDIFTGEPSSLDPSP 120
DB 61 DEETNDVPHIQCGDQDPOGLRDNQFCLQRIHQGLIFYEKLGLSDIFTGEPSSLDPSP 120

QY 121 VAQLHASLGLSLLQQLQPEGHWHWTQOIPSLSPSQPWQRLRLFRKILRSLOAFVAVARVF 180
DB 121 VQLHASLGLSLLQQLQPEGHWHWTQOIPSLSPSQPWQRLRLFRKILRSLOAFVAVARVF 180

QY 181 AHGAATLSP 189
DB 181 AHGAATLSP 189

RESULT 14

AAV54606
ID AAV54606 standard; protein; 189 AA.

XX AAV54606;

XX 01-FEB-2000 (first entry)

XX SGRF protein sequence.

XX SGRF; human; Interleukin-6 G-CSF related factor; cell proliferation;
KW immune system; haematopoietic system; therapy.

XX Homo sapiens.

XX WO9543357-A1.

XX 28-OCT-1999.

XX 14-APR-1999; 99WO-JP001997.

XX 14-APR-1998; 98JP-00121805.

XX (CHUS) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX Hirata Y;

XX WPI; 2000-013230/01.

XX N-PSDB; AAZ37262, AAZ37263.

XX Novel cytokine-like protein, with activity of supporting proliferation of
PT myeloid cells, useful in treating abnormality of cell proliferation in
PT immune and hematopoiesis systems.

XX Claim 1; Fig 1; 69pp; Japanese.

CC This sequence is the Interleukin-6 G-CSF related factor (SGRF) protein of
CC the invention. The protein is a member of the IL-6/G-CSF/MSF family. The
CC protein can be used in drugs for treating diseases due to abnormality of
CC cell proliferation in the immune system and haematopoietic system

XX Sequence 189 AA;

Query Match 99.6%; Score 1000; DB 3; Length 189;
Best Local Similarity 99.5%; Pred. No. 1.6e-96;
Matches 188; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGSRVAVMLLLPWTAGRAVPGSSPAWTCQQLSQKLTLSAHPVGHMDLREEG 60
DB 1 MGSRVAVMLLLPWTAGRAVPGSSPAWTCQQLSQKLTLSAHPVGHMDLREEG 60

QY 61 DEETNDVPHIQCGDQDPOGLRDNQFCLQRIHQGLIFYEKLGLSDIFTGEPSSLDPSP 120
DB 61 DEETNDVPHIQCGDQDPOGLRDNQFCLQRIHQGLIFYEKLGLSDIFTGEPSSLDPSP 120

QY 121 VAQLHASLGLSLLQQLQPEGHWHWTQOIPSLSPSQPWQRLRLFRKILRSLOAFVAVARVF 180
DB 121 VQLHASLGLSLLQQLQPEGHWHWTQOIPSLSPSQPWQRLRLFRKILRSLOAFVAVARVF 180

QY 181 AHGAATLSP 189

DB 181 AHGAATLSP 189

RESULT 15

AAU12287

ID AAU12287 standard; protein; 189 AA.

XX AAU12287;

XX 24-OCT-2001 (first entry)

XX Human PRO5798 polypeptide sequence.

XX Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW A-peptide; factor VIIA; gene therapy.

XX Homo sapiens.

XX WO2000140466-A2.

XX 07-JUN-2001.

XX 01-DEC-2000; 2000WO-US032678.

XX 01-DEC-1999; 99WO-US028301.

XX 01-DEC-1999; 99WO-US028634.

XX 02-DEC-1999; 99WO-US028551.

XX 02-DEC-1999; 99WO-US028564.

XX 02-DEC-1999; 99WO-US028565.

XX 09-DEC-1999; 99US-0170262P.

XX 16-DEC-1999; 99WO-US030095.

XX 20-DEC-1999; 99WO-US030911.

XX 30-DEC-1999; 99WO-US031243.

XX 30-DEC-1999; 99WO-US031274.

XX 05-JAN-2000; 2000WO-US000219.

XX 06-JAN-2000; 2000WO-US000277.

XX 11-FEB-2000; 2000WO-US000376.

XX 18-FEB-2000; 2000WO-US004341.

XX 18-FEB-2000; 2000WO-US004342.

XX 22-FEB-2000; 2000WO-US004414.

XX 24-FEB-2000; 2000WO-US004914.

XX 01-MAR-2000; 2000WO-US005004.

XX 02-MAR-2000; 2000WO-US005601.

XX 02-MAR-2000; 2000WO-US005841.

PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.

XX (GETH) GENENTECH INC.

XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX

DR WPI; 2001-408281/43.
DR N-PSDB; AAS21359.

XX Isolated , secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT breast, prostate, cervical.

XX Claim 12; Fig 232; 813pp; English.

XX AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
CC polypeptides. The PRO polypeptides are useful to detect other PRO
CC polypeptides, to link bioactive molecules to cells expressing PRO
CC polypeptides, to modulate biological activities of cells expressing PRO
CC polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample. Some
CC of the 275 sequences are also useful to stimulate the release of tumour
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC differentiation of chondrocytes, the release of proteoglycans from cartilage, the
CC pericyte cells, the release of proteoglycans from cartilage, the
CC proliferation of inner ear utricular supporting cells or of T-
CC lymphocytes, the release of a cytokine from peripheral blood monocytes
CC (BMCs) or the proliferation of endothelial cells. Some of the PRO
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC VIIA. The PRO polypeptides can be used in assays to identify molecules
CC involved in binding interactions. The polynucleotides encoding PRO
CC polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy
XX

SQ Sequence 189 AA;

Query Match 99.6%; Score 1000; DB 4; Length 189;
Best Local Similarity 99.5%; Pred. No. 1.6e-96;
Matches 188, Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLGSRAVMLLLLLPWTAGRAVPGSSPAWTCQOOLSQKLTAWSAHPLVGHMDLREEG 60
Db 1 MLGSRAVMLLLLLPWTAGRAVPGSSPAWTCQOOLSQKLTAWSAHPLVGHMDLREEG 60
Qy 61 DEETTNDVPHIQCGDGDPOGLRDNQFCQRIHQGLIFYEKLGSDIFTGEPSPDPS 120
Db 61 DEETTNDVPHIQCGDGDPOGLRDNQFCQRIHQGLIFYEKLGSDIFTGEPSPDPS 120
Qy 121 VAQLHASLLGLSQQLPEGHHWETQIQIPSLSPSPQWQRLRLFRKILRSLOAFVAVARVF 180
Db 121 VGQLHASLLGLSQQLPEGHHWETQIQIPSLSPSPQWQRLRLFRKILRSLOAFVAVARVF 180

Qy 181 AHGAATLSP 189
Db 181 AHGAATLSP 189

Search completed: June 20, 2006, 04:32:11
Job time : 301.555 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2006, 04:32:40 ; Search time 25.0364 Seconds
(without alignments)
726.342 Million cell updates/sec

Title: US-10-797-157-2
Perfect score: 1004
Sequence: 1 MLGSRVNLMLLLPWTAGR.....QAFVAVARVFAHGATLSP 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100	10.0	204	1 FQHUGL	granulocyte colony
2	99.5	9.9	194	2 T09255	granulocyte colony
3	91	9.1	208	1 S29549	interleukin-6 - sh
4	90.5	9.0	174	2 T10268	granulocyte colony
5	88.5	8.8	207	2 A24573	granulocyte colony
6	87.5	8.7	208	2 A26496	granulocyte colony
7	86	8.6	1121	2 A82809	exodeoxyribonuclea
8	85	8.5	211	1 ICMS6	interleukin-6 prec
9	80.5	8.0	232	2 D70537	hypothetical prote
10	80.5	8.0	530	2 D96810	hypothetical prote
11	80	8.0	858	2 JC7683	taste receptor T1R
12	79.5	7.9	201	2 A42247	myelomonocytic gro
13	79	7.9	506	2 AG0893	aerotaxis receptor
14	79	7.9	2512	1 XYCHFA	enoyl-lacetyl-carrie
15	78	7.8	1026	2 T05882	hypothetical prote
16	77.5	7.7	513	2 C82366	conserved hypothet
17	77.5	7.7	967	2 G86229	hypothetical prote
18	76.5	7.6	399	2 A11929	N-acetyl-glucosami
19	76.5	7.6	881	2 F84404	valyl-tRNA synthet
20	76	7.6	262	2 A84240	molybdopterin oxid
21	75.5	7.5	214	2 JC5043	granulocyte colony
22	75.5	7.5	265	2 B83395	probable enoyl-CoA
23	75.5	7.5	938	2 A56731	chromatin assembly
24	75.5	7.5	2304	2 T07920	probable acetyl-Co
25	75	7.5	195	2 I47070	interferon omega -
26	75	7.5	211	2 A34247	interleukin-6 prec
27	75	7.5	801	1 S00943	glucose dehydrogen
28	75	7.5	975	2 T48107	hypothetical prote
29	74.5	7.4	212	2 I48590	interleukin 6 - pi

30	74.5	7.4	212	2 I46621	prointerleukin 6 -
31	74.5	7.4	280	2 S75845	hypothetical prote
32	74	7.4	314	2 T27137	hypothetical prote
33	74	7.4	374	2 T26739	hypothetical prote
34	74	7.4	974	2 A86263	Flk23.18 protein
35	74	7.4	1148	2 AD0198	transcription-repa
36	73.5	7.3	247	2 H70916	probable glucose-6
37	73.5	7.3	310	2 B90696	probable glutamina
38	73.5	7.3	310	2 F85546	probable glutamina
39	73.5	7.3	649	2 T04005	probable protein k
40	73.5	7.3	755	2 D75598	photoreceptor - de
41	73.5	7.3	1015	2 I39697	beta-galactosidase
42	73	7.3	346	2 A58583	testosterone-resis
43	73	7.3	462	2 A12319	UDP-N-acetylmuram
44	72.5	7.2	259	2 T28147	class II histocomp
45	72.5	7.2	374	2 C98215	oligopeptide ABC t

ALIGNMENTS

RESULT 1

FOHUGL

granulocyte colony-stimulating factor precursor - human
N:Alternate names: colony-stimulating factor 3; G-CSF
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1988 #sequence revision 18-Aug-1995 #text_change 09-Jul-2004
C:Accession: A25093; A49796; A47587; S68331
R:Nagata, S.; Tsuchiya, M.; Asano, S.; Yamamoto, O.; Hirata, Y.; Kubota, N.; Oheda, M.;
EMBO J. 5, 575-581, 1986
A:Title: The chromosomal gene structure and two mRNAs for human granulocyte colony-stim
A:Reference number: A25093; MUID:86220137; PMID:2423327
A:Accession: A25093
A:Molecule type: DNA; mRNA
A:Residues: 1-204 <NAG>
A:Cross-references: UNIPROT:P09919; UNIPARC:UPI000002A734; EMBL:X03656; EMBL:X03655; NIT
R:Devlin, J.J.; Devlin, P.E.; Myambo, K.; Lilly, M.B.; Rado, T.A.; Warren, M.K.
J. Leukoc. Biol. 41, 302-306, 1987
A:Title: Expression of granulocyte colony-stimulating factor by human cell lines.
A:Reference number: A49796; MUID:87196936; PMID:3494801
A:Accession: A49796
A:Molecule type: mRNA
A:Residues: 1-204 <DEV>
A:Cross-references: UNIPARC:UPI000002A734; GB:M17706; NID:q183040; PIDN:AAA35882.1; PID
R:Souza, L.M.; Boone, T.C.; Gabrilove, J.; Lai, P.H.; Zaebo, K.M.; Murdock, D.C.; Chazi

Science 232, 61-65, 1986
A:Title: Recombinant human granulocyte colony-stimulating factor: effects on normal and
A:Reference number: A47587; MUID:86151684; PMID:2420009
A:Accession: A47587
A:Molecule type: mRNA
A:Residues: 19-204 <SOU>
A:Cross-references: UNIPARC:UPI0000158376; GB:M13008; NID:q183044; PIDN:AAA03056.1; PID
R:Haniu, M.; Horan, T.; Arakawa, T.; Le, J.; Katta, V.; Rohde, M.F.
Arch. Biochem. Biophys. 324, 344-356, 1995
A:Title: Extracellular domain of granulocyte-colony stimulating factor receptor.
A:Reference number: S68331; MUID:96132662; PMID:8554326
A:Accession: S68331
A:Molecule type: protein
A:Residues: 'M',31-46 <HAN>
A:Cross-references: UNIPARC:UPI0000173677
C:Genetics:
A:Gene: GDB:CSF3
A:Cross-references: GDB:119083; OMIM:138970
A:Map position: 17q11.2-17q12
A:Introns: 14/1; 65/3; 101/3; 150/3
C:Function:
A:Description: stimulates the differentiation and proliferation of hematopoietic progeni
A:Superfamily: interleukin-6
C:Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-204/Product: granulocyte colony-stimulating factor #status predicted <MAT>
F:66-72,94-104/Disulfide bonds: #status predicted

A;Residues: 31-34, 'X', 36-43;48-51, 'X', 53-57; 'X', 60-71;159-164, 'X', 166-176;183-198, 'X', 21, 22;
A;Cross-references: UNIPARC:UPI0000176729; UNIPARC:UPI000017672A; UNIPARC:UPI000017672B;
C;Genetics:
A;Introns: 14/1; 71/3; 107/3; 156/3
C;Superfamily: interleukin-6
C;Keywords: cytokine; growth factor; macrophage; monomer

Query Match 8.7%; Score 87.5; DB 2; Length 208;
Best Local Similarity 25.0%; Pred. No. 0.79;
Matches 41; Conservative 23; Mismatches 59; Indels 41; Gaps 10;

Qy 36 LSKKLTCLAWSNHP-----LVGHMDLREEGDEETNDVPHIQCGDGPQGLRDNSSQFCLO 91
Db 67 LLEQLCATYKCHPEELVLLGH-----SLGIPKASL-SGCSQALQOTQ--CLS 112

Qy 92 RIHQGLIYEKLLGSDIFGT-EPSSLDPSPVAQLHAS-----LGLLSOLLOPEG 139
Db 113 QHSHGLCLYQGLL--QALSGTSPALAPTLDLQLDQVANFATTIQQMENLGVAPTQVP-- 168

Qy 140 HHWTQQ-IPSLSPSPQWQRLRLLRKILRSLOAFVAARVFAH 182
Db 169 ---TQSAMPATSA--FORRAGGVLAISYLOQGFLETARLALHH 206

RESULT 7
ex02009
A;Cross-references: UNIPROT:O9PG80; UNIPARC:UPI00000C23E1; GB:AE003893; GB:AE003849; NID
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: A82809
F;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: A82809
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1121 <SIM>
A;Cross-references: UNIPROT:O9PG80; UNIPARC:UPI00000C23E1; GB:AE003893; GB:AE003849; NID
F;Experimental source: strain 9A5C
F;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF0422

Query Match 8.6%; Score 86; DB 2; Length 1121;
Best Local Similarity 23.7%; Pred. No. 8;
Matches 41; Conservative 18; Mismatches 56; Indels 58; Gaps 9;

Qy 22 VPGSSPAWTCQQLSQKL-----CTL-----AWSA-----HPLVGHMDLREEGDE 62
Db 236 LPTPTKEVGDRAQPTQRLHQFTDCVTQGENLLHAWGNAGRDFMTVLGSYEVVHPSGE 295

Qy 63 ETTNDVPHIQCGDGPQGLRDNSSQFCLORIHQGLIFYEKLGLSDIFGT-----PSLLP- 117
Db 296 ITAYDDPEQRLGTTLDEGLRDS--LLQRMH-----ADLFHNSAPVPAPLPA 341

Qy 118 ---DSPVAQLHASLGLSOLL-----QPEGHWTQQIIFSLSPSQ 154
Db 342 PRLEDPSLQFACHTFLRLQLVHLHDLRALLEPNSPEGRFN-----PPLQPRE 390

A;Residues: 1-211 <CHI>
A;Cross-references: UNIPARC:UPI0000029AF5; GB:J03783; NID:g198367; PIDN:AAA39301.1; PID:
R;Shabo, Y.; Lotem, J.; Rubinstein, M.; Revel, M.; Clark, S.C.; Wolf, S.F.; Kamen, R.; S.
Blood 72, 2070-2073, 1988
A>Title: The myeloid blood cell differentiation-inducing protein MGI-2A is interleukin-6
A;Reference number: A50799; MUID:89062753; PMID:3264198
A;Accession: A60799
A:Molecule type: protein
A;Residues: 77-98 <SHA>
A;Cross-references: UNIPARC:UPI0000173673
R;Blankenstein, T.; Qin, Z.; Li, W.; Diamantstein, T.
J. Exp. Med. 171, 965-970, 1990
A>Title: DNA rearrangement and constitutive expression of the interleukin 6 gene in a mo
A;Reference number: SI0241; MUID:90171860; PMID:2106369
A;Accession: SI0241
A>Status: preliminary
A:Molecule type: DNA
A;Residues: 1-6 <BLA>
A;Cross-references: UNIPARC:UPI000016CB67; EMBL:X51457; NID:g49738; PIDN:CAA35824.1; PID:
E;Zhang, J.G.; Reid, G.E.; Moricz, R.L.; Ward, L.D.; Simpson, R.J.
Eur. J. Biochem. 217, 53-59, 1993
A>Title: Specific covalent modification of the tryptophan residues in murine interleukin
A;Reference number: S38254; MUID:94039075; PMID:8223586
A;Accession: S38254
A>Status: preliminary
A:Molecule type: protein
A;Residues: 38-60'75,'X', 77-79;176-203 <ZHA>
A;Cross-references: UNIPARC:UPI0000173674; UNIPARC:UPI0000173675; UNIPARC:UPI0000173676
C;Genetics:
A;Gene: IL-6
A;Map position: 5
A;Introns: 7/1; 68/3; 106/3; 156/3
C;Superfamily: interleukin-6
C;Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine;
F;1-24/Domain: signal sequence #status predicted <Sig>
F;25-211/Product: interleukin-6 #status experimental <Mat>

Query Match 8.5%; Score 85; DB 1; Length 211;
Best Local Similarity 22.9%; Pred. No. 1.4;
Matches 44; Conservative 20; Mismatches 58; Indels 70; Gaps 9;

Qy	28	PAWTQCQ-----QLSQKCLTAWSAHPLVGHMDLRBEGDEETND--VPHIQ 72
	:	: :
Dd	44	PVYTTSQGGIITHVLWEIVEMRKELCN-----GNSDCMNDDALAEENLKLPFIQ 94
	:	: :
Qy	73	CGDCCDPGLDRNSFCQRTHOGLIFYE-----KLIGSD-----I 108
	:	: :
Dd	95	RNDSCYQTGY--NQEICLLKTSGLLEHSYLEYMKNNLNKKDKKARVLORDTETLIHI 152
	:	: :
Qy	109	PTGEPSLLPDSFVAQLHASLI--GLSQLQPFGHHWETOQIPSLSPSQPWQRLLRPKIL 166
	:	: :
Dd	153	FNQE-----VKDLHKIVLPTISPALLTD-----KLESQKEWLRTKTIOFIL 194
	:	: :
Qy	167	RSLOAFVAVAAR 178
	:	: :
Dd	195	KSLSEFLKVTLUR 206
	:	: :

RESULT 9
D70537
hypothetical protein Rvll15 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: D70537
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrall, B.G.
A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70537
A>Status: preliminary; nucleic acid sequence not shown; translation not shown


```
Db      79 PHLVQAPLDQCHKRGFQ--AEVCFQTRAGLHAYHDSLGAVL-----RLLPNHTTLVETL 131
Qy      123 QLHASLLGLSLLQPEGHWHWTQIPSS--LSP-----SOPWQRLRLRFKILRSLOAFVAVA 176
Db      132 QLDANLSSNIQQQMEDLGLDVTILPAEQRSPPPTFSGPFQQVGGFFILANFORFLETA 191
Qy      177 ARVFAH 182
Db      192 YRALRH 197

RESULT 13
AG0893
aerotaxis receptor protein [imported] - Salmonella enterica subsp. enterica serovar Typh
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AG0893
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AG0893
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-506 <PAR>
A:Cross-references: UNIPARC:UPI000005A4B3; GB:AL513382; PIDN:CAD07741.1; PID:gl6504293;
C:Genetics: STY3395
C:Superfamily: methyl-accepting chemotaxis protein

Query Match 7.9%; Score 79; DB 2; Length 506;
Best Local Similarity 21.3%; Pred. No. 14;
Matches 40; Conservative 19; Mismatches 55; Indels 74; Gaps 6;

Qy      48 HPLVGHMDL-----REEGDE--ETTNDVPHIQCGDGDQPQ 80
Db      53 HNLVRHDPKCAAFADMMWYTLKQEPWSGIVKRNKGDHVVWVANAVPMIREGRVTGYM 112
Qy      81 GLRD-----NSQFCLORIHQGLIFYEKLGISDIFTGEPSELDPSPVAQ 123
Db      113 SIRTRATDDETAAVEPLYQALNEGRCSKRIHKGVLVVRQGLGK-----LPAMPVRW 163
Qy      124 LHASLLGLSLLQPEGHWHWTQIPSLSPSPQWQRLLL-----RFLKILRSLOA 171
Db      164 RVRSIMGLMAVM-----LALALFGTASWQALLGLGALMLAGTALFEWQIVRFPIEN 214
Qy      172 FVAVAARV 179
Db      215 VATQALKV 222

RESULT 14
XYCHFA
enoyl-[acyl-carrier-protein] reductase (NADPH2, B-specific) (EC 1.3.1.10) - chicken
N:Contains: 3-hydroxypalmitoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.61); 3-oxoa
cyl-[acyl-carrier-protein] reductase (NADPH, B-specific) (EC 1.3.1.10); oleoyl-[acyl-car
protein] S-malonyltransferase (EC 2.3.1.39)
C:Species: Gallus gallus (chicken)
C:Date: 30-Sep-1991 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C:Accession: S57248; S51519; A30620; A29967; A33918; A30445; A31236; B31236; A30297; A31
R;Huang, W.Y.; Chirala, S.S.; Wakil, S.J.
submitted to the EMBL Data Library, January 1989
A:Description: Amino-terminal blocking group and sequence of the animal fatty acid synth
A:Reference number: S57248
A:Accession: S57248
A:Molecule type: mRNA
A:Residues: 1-2512 <HUA1>
A:Cross-references: UNIPROT:P12276; UNIPARC:UPI0000017131B; EMBL:J04485; NID:9460908; PID
```

```
R;Huang, W.Y.; Chirala, S.S.; Wakil, S.J.
Arch. Biochem. Biophys. 314, 45-49, 1994
A:Title: Amino-terminal blocking group and sequence of the animal fatty acid synthase.
A:Reference number: S51519; MUID:95031085; PMID:7944406
A:Accession: S51519
A:Molecule type: mRNA
A:Residues: 1-182 <HUA2>
A:Cross-references: UNIPARC:UPI000001723D9; EMBL:J04485; NID:9460908
A:Accession: A30620
A:Molecule type: protein
A:Residues: 1-12 <HUA3>
A:Cross-references: UNIPARC:UPI000001723DA
R;Chang, S.I.; Hammes, G.G.
Biochemistry 27, 4753-4760, 1988
A:Title: Amino acid sequences of substrate-binding sites in chicken liver fatty acid syr
A:Reference number: A29967; MUID:89000676; PMID:3167014
A:Accession: A29967
A:Molecule type: protein
A:Residues: 144-166:575-583;2141-2165 <CHAI>
A:Cross-references: UNIPARC:UPI000001723DB; UNIPARC:UPI000001723DC; UNIPARC:UPI000001723DD
R;Holzer, K.P.; Liu, W.; Hammes, G.G.
Proc. Natl. Acad. Sci. U.S.A. 86, 4387-4391, 1989
A:Title: Molecular cloning and sequencing of chicken liver fatty acid synthase cDNA.
A:Reference number: A33918; MUID:89282777; PMID:2734291
A:Accession: A33918
A:Molecule type: mRNA
A:Residues: 75-77,'PV',80-116,'A',118-675,'S',677-1169,'N',1171-1178,'T',1180-1191,'H',1
L>
A:Cross-references: UNIPARC:UPI000001723DE
A:Accession: A30445
A:Molecule type: protein
A:Residues: 107-113;1086-1091 <HOL1>
A:Cross-references: UNIPARC:UPI000001723DE
R;Yuan, Z.; Liu, W.; Hammes, G.G.
Proc. Natl. Acad. Sci. U.S.A. 85, 6328-6331, 1988
A:Title: Molecular cloning and sequencing of DNA complementary to chicken liver fatty ac
A:Reference number: A31236; MUID:88320436; PMID:2842766
A:Accession: A31236
A:Molecule type: mRNA
A:Residues: 1752-2350,'CFSPSLFO',2351-2512 <YUA1>
A:Cross-references: UNIPARC:UPI000001723E1
A:Accession: B31236
A:Molecule type: mRNA
A:Residues: 1752-2512 <YUA2>
A:Cross-references: UNIPARC:UPI000001723E1; GB:J03860; GB:M22987; NID:g211766
A:Note: neither the complete nucleic acid sequence nor the complete translation are show
R;Chirala, S.S.; Kasturi, R.; Pazirandeh, M.; Stollow, D.T.; Huang, W.Y.; Wakil, S.J.
J. Biol. Chem. 264, 3750-3757, 1989
A:Title: A novel cDNA extension procedure. Isolation of chicken fatty acid synthase cDNA
A:Reference number: A30297; MUID:89139426; PMID:2917973
A:Accession: A30297
A:Molecule type: mRNA
A:Residues: 1568-2512 <CHI>
A:Cross-references: UNIPARC:UPI000001723E3; EMBL:J04485; NID:9460908
A:Note: neither the complete nucleic acid sequence nor the complete translation are show
R;Yang, C.Y.; Huang, W.Y.; Chirala, S.; Wakil, S.J.
Biochemistry 27, 7773-7777, 1988
A:Title: Complete amino acid sequence of the thioesterase domain of chicken liver fatty
A:Reference number: A31184; MUID:89088151; PMID:3207709
A:Accession: A31184
A:Molecule type: protein
A:Residues: 2209-2508 <YAN>
A:Cross-references: UNIPARC:UPI000001723E4
R;Kasturi, R.; Chirala, S.; Pazirandeh, M.; Wakil, S.J.
Biochemistry 27, 7778-7785, 1988
A:Title: Characterization of a genomic and cDNA clone coding for the thioesterase domain
A:Reference number: A31185; MUID:89088152; PMID:3207710
A:Accession: A31185
A:Molecule type: DNA
A:Residues: 2202-2512 <KASI>
A:Cross-references: UNIPARC:UPI000001723E5; EMBL:J02839; NID:g211768; PID:AAA82106.1; PI1
A:Accession: A30446
```

[illegible]

RESULT 15 .
T05882
hypothetical protein FGH11.10 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 09-Jul-2004
C:Accession: T05882
R:Bevan, M.; Brandt, P.; Dose, S.; Jarke, D.; Scharfe, M.; Schon, O.; Bancroft, C.
submitted to the Protein Sequence Database, April 1998
A:Reference number: Z15456
A:Accession: T05882
A:Molecule type: DNA
A:Residues: 1-1026 <BEV>
A:Cross-references: UNIPROT:O49529; UNIPARC:UPI00000A2380; EMBL:AL021684
A:Experimental source: cultivar Columbia; BAC clone FGH11
C:Genetics:
A:Map position: 5
A:Introns: 37/2; 109/1; 115/2; 560/1; 737/1; 833/3
A:Note: FGH11.10

Query Match	7.8%;	Score 78;	DB 2;	Length 1026;
Best Local Similarity	22.9%;	Pred. No. 40;		
Matches	30;	Conservative 18;	Mismatches 53;	Indels 30; Gaps 4;
Qy	2	LGSRVWLLLLLFWTAGRAVPGSSPAWTCQOQLSKLCTL-----AWSAHP	49	
Db	518	VGLAAKLLV-----IQSGDPALKQRSAELLKCLSHYSMSFTSKYMWLARS	567	
Qy	50	LVGHMDLRE--EGDEETTNDVPHIQCGDGDPOGLRDNSQFCILQRIHQGLIFYEKLIGSD	107	
Db	568	IANSKLDEDEDDKHLNQPPSEVSQSPRGVKEDISELTKTLR-----TQFWGVA	621	
Qy	108	IFTGEPSSLDP	118	
Db	622	SFLSQPSSSPD	632	

Search completed: June 20, 2006, 04:40:21
Job time : 29.0364 secs

Query Match 7.9%; Score 79; DB 1; Length 2512;

THIS PAGE BLANK (USPTO)

GenCore version 5.1.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2006, 04:22:58 ; Search time 209.127 Seconds
(without alignments)
835.988 Million cell updates/sec

Title: US-10-797-157-2

Perfect score: 1004

Sequence: 1 MLGSAVMLLLPWTAGR.....QAFVAVARFAHGAATLSP 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 92501592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1004	100.0	189	2	Q9H2A5 HUMAN
2	1000	99.6	189	2	Q9NPF7 HUMAN
3	994	99.0	189	2	Q6NZ82 HUMAN
4	989	98.5	189	2	Q6NZ80 HUMAN
5	873.5	87.0	192	2	Q64FUL HORSE
6	846	84.3	193	2	Q9N2H9 PIG
7	819	81.6	189	2	Q6LA37 CAVPO
8	799.5	79.6	185	2	Q2Q586 FELCA
9	784.5	78.1	196	2	Q91284 RAT
10	768	76.5	184	2	Q8QWE2 PERMA
11	718.5	71.6	196	2	Q9SQ14 MOUSE
12	107	10.7	236	2	Q516V9 ENTHI
13	106.5	10.6	195	1	CSF3 FIG
14	102	10.2	200	2	Q8N4W3 HUMAN
15	100	10.0	204	2	Q6FH65 HUMAN
16	99.5	9.9	194	1	CSF3 FELCA
17	97	9.7	195	2	Q9GUU0 FELCA
18	96	9.6	208	1	IL6 SHEEP
19	96	9.6	454	2	Q5FR22 PONPY
20	94	9.4	199	2	Q7SX81 FUGRU
21	92.5	9.2	249	2	Q3W0K9 ACTO
22	92	9.2	196	2	Q2EDJ1 FUGRU
23	90.5	9.0	174	1	CSF3 SHEEP
24	89.5	8.9	175	1	CSF3 CANFA
25	89	8.9	208	1	IL6 CAPHI
26	88.5	8.8	207	1	CSF3 HUMAN
27	87.5	8.7	208	1	CSF3 MOUSE
28	87	8.7	816	2	Q5N580 SYNPF
29	87	8.7	822	2	Q31NY7 SYNPF
30	86.5	8.6	208	2	Q3UM22 MOUSE
31	86.5	8.6	996	2	Q4SCJ1 TETNG

32	86	8.6	418	2	Q2N2P6 AERHY	Q2n2p6 aeromonas h
33	86	8.6	482	2	Q3H179 TRIER	Q3h179 trichodesmi
34	86	8.6	1121	2	Q9PG80_XYLFA	Q9pg80 xylella fas
35	85.5	8.5	352	2	Q9PZ44_9RETR	Q9pz44 multiple sc
36	85.5	8.5	362	1	GAW2_HUMAN	Q9nrz4 homo sapien
37	85	8.5	101	2	Q7S138_ORYSA	Q7s138 oryza sativ
38	85	8.5	194	2	Q3U8J8_MOUSE	Q3u8j8 mus musculu
39	85	8.5	211	1	IL6_MOUSE	P08505 mus musculu
40	85	8.5	211	2	Q3UCQ0_MOUSE	Q3ucq0 mus musculu
41	85	8.5	454	2	Q68D85_HUMAN	Q68d85 homo sapien
42	85	8.5	520	2	Q723M6_HUMAN	Q723m6 homo sapien
43	85	8.5	1121	2	Q3RHS2_XYLFA	Q3rhz2 xylella fas
44	85	8.5	1121	2	Q3RHS2_XYLFA	Q3rhz2 xylella fas
45	84.5	8.4	210	2	Q9WVQ8_MBSAU	Q9wvq8 mesocricetu

ALIGNMENTS

RESULT 1
Q9H2A5_HUMAN PRELIMINARY; PRT; 189 AA.
AC Q9H2A5;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DE 07-FEB-2006, entry version 16.
DE Interleukin 23 p19 subunit.
GN Name=IL23A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
RX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20567322; PubMed=11114383; DOI=10.1016/S1074-7613(00)00070-4;
RA Oppmann B., Lesley R., Blom B., Timans J.C., Xu Y., Hunte B., Vega F.,
RA Yu N., Wang J., Singh K., Zonin F., Vaisberg E., Churakova T.,
RA Liu M.-R., Gorman D., Wagner J., Zurawski S., Liu Y.-J., Abrams J.S.,
RA Moore K.W., Rennick D., de Waal-Malefyt R., Hannum C., Bazan J.F.,
RA Kastelein R.A.;
RT "Novel p19 protein engages IL-12p40 to form a cytokine, IL-23, with
biological activities similar as well as distinct from IL-12.";
RL Immunity 13:715-725(2000).
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs license

CC EMBL; AF301620; AAG37232.1; -, mRNA.
DR Ensembl; ENSG00000110944; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPRO12351; Cytokine_4_hlx.
DR InterPro; IPRO10831; IL23A.
DR InterPro; IPRO03573; IL6 MGF GCSF.
DR PANTHER; PTHR15947; IL23A; 1.
DR Pfam; PF00489; IL6; 1.
SQ SEQUENCE 189 AA; 20744 MW; BFB5C0F42D4C1E3A CRC64;

Query Match 100.0%; Score 1004; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 2.2e-84;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MLGSAVMLLLPWTAGRAVPGSSPAWTCQQLSQKLCITLAWSAHPLVGHMDLREEG 60	
Db	1	MLGSAVMLLLPWTAGRAVPGSSPAWTCQQLSQKLCITLAWSAHPLVGHMDLREEG 60	
QY	61	DEETNDVPHICGGCDPQGLRDNQFCQLQRIHQGLIEYKLGSDIFTGSPSLPDSP 120	
Db	61	DEETNDVPHICGGCDPQGLRDNQFCQLQRIHQGLIEYKLGSDIFTGSPSLPDSP 120	
QY	121	VAQLHASLLGLSQLLPQEGHHWETQIIFSLSPSPQWRLLLRKILRSLOAFVAAARVF 180	

```

Db 121 VAQLHASLLGLSQQLOPEGHWHWTQIIPSLSPSQWQRLRLFKILRSLOAFVAAARVF 180
QY 181 AHGAATLSP 189
Db 181 AHGAATLSP 189

RESULT 2
Q9NPF7_HUMAN
ID Q9NPF7_HUMAN PRELIMINARY; PRT; 189 AA.
AC Q9NPF7;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE SGRF precursor (IL-23 p19) (Interleukin 23, alpha subunit p19).
GN Name=SGRF; Synonyms=IL23A; ORFNames=UNQ2498;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=SPLEEN;
RC Hirata Y., Kosuge Y.;
RT "SGRF, a novel member of the IL-6/G-CSF family,";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vanden R.L., Watanabe C., Weand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
[3]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshlyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Wozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[4]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=PCR rescued clones;
RA Director MGC Project;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

```

```

RN NUCLEOTIDE SEQUENCE.
RP TISSUE=PCR rescued clones;
RA Strausberg R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
[5]
DR EMBL; AB030000; BAA93686.1; -; mRNA.
DR EMBL; AY359083; AAQ89442.1; -; mRNA.
DR EMBL; BC066268; AAH6268.1; -; mRNA.
DR EMBL; BC067511; AAH67511.1; -; mRNA.
DR EMBL; BC067512; AAH67512.1; -; mRNA.
DR EMBL; BC067513; AAH67513.1; -; mRNA.
DR EMBL; AB030001; BAA93687.1; -; Genomic DNA.
DR Ensembl; ENSG00000110944; Homo sapiens.
DR GO; GO:000576; C:extracellular region; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR010831; IL23A.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR PANTHER; PTHR15947; IL23A; 1.
DR Pfam; PF00489; IL6; 1.
KW Signal.
FT SIGNAL
FT CHAIN
SQ SEQUENCE 189 AA; 20730 MW; 51B5C0F188EC1B9F CRC64;
Query Match 99.6%; Score 1000; DB 2; Length 189;
Best Local Similarity 99.5%; Pred. No. 5.2e-84;
Matches 188; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLGSRAVMLLLPWTAAQGRAVPGGSSPAWTQQQQLSOKLCTLAWSAHLVGHMDLREEG 60
DB 1 MLGSRAVMLLLPWTAAQGRAVPGGSSPAWTQQQQLSOKLCTLAWSAHLVGHMDLREEG 60
QY 61 DEETTNDVPHIQCGDGPQGLRDNSQFCILQRIHQGLIFVEYKLGSDIFTGEPSSLDPSP 120
DB 61 DEETTNDVPHIQCGDGPQGLRDNSQFCILQRIHQGLIFVEYKLGSDIFTGEPSSLDPSP 120
QY 121 VAQLHASLLGLSQQLOPEGHWHWTQIIPSLSPSQWQRLRLFKILRSLOAFVAAARVF 180
DB 121 VAQLHASLLGLSQQLOPEGHWHWTQIIPSLSPSQWQRLRLFKILRSLOAFVAAARVF 180
QY 181 AHGAATLSP 189
DB 181 AHGAATLSP 189

RESULT 3
Q6NZ82_HUMAN
ID Q6NZ82_HUMAN PRELIMINARY; PRT; 189 AA.
AC Q6NZ82;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Interleukin 23, alpha subunit p19.
GN Name=IL23A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshlyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Wozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[4]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=PCR rescued clones;
RA Director MGC Project;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

```

NUCLEOTIDE SEQUENCE.

RP TISSUE=PCR rescued clones;
RC MEDLINE=42388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Pange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallatou D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krywinski M.I., Skalska J., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RA Director MGC Project;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBSJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
CC EMBL: BC066269; AAH66269.1; -; mRNA.
DR Ensembl: ENSG00000110944; Homo sapiens.
DR HGNC: HGNC:15488; IL23A.
DR GO: GO:0005576; C:extracellular region; IEA.
DR GO: GO:0005125; F:cytokine activity; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR InterPro: IPR012351; Cytokine_4_hlx.
DR InterPro: IPR010831; IL23A.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR PANTHER: PTHR15947; IL23A; 1.
DR Pfam: PF00489; IL6; 1.
SQ SEQUENCE 189 AA; 20718 MW; 594290F188EC1B9F CRC64;

Query Match 98.5%; Score 989; DB 2; Length 189;
Best Local Similarity 98.9%; Pred. No. 5.4e-83;
Matches 186; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 1 MLGSRAVMLLLLPWTQAQRAVPGGSSPAWTCQQLSQKSLCTLAWSAHLVGHMDLREG 60
Db 1 MLGSRAVMLLLLPWTQAQRAVPGGSSPAWTCQQLSQKSLCTLAWSAHLVGHMDLREG 60
QY 61 DEETNDVPHIQCGDGDPCQGLRDNDSQFCLQRIHQGLIFYEKLGLSDIFTGSPSLPDS 120
Db 61 DEETNDVPHIQCGDGDPCQGLRDNDSQFCLQRIHQGLIFYEKLGLSDIFTGSPSLPDS 120
QY 121 VAQLHASLLGLSQLOPEGHWHWTQQIPSLSPSPQWQLLRFLKILRSLOAFVAARVF 180
Db 121 VQGLHASLLGLSQLOPEGHWHWTQQIPSLSPSPQWQLLRFLKILRSLOAFVAARVF 180
QY 181 AHGAATLS 188
Db 181 AHGAATLS:188

RESULT 5
Q64FUI_HORSE
ID Q64FUI_HORSE PRELIMINARY; . PRT; 192 AA.
AC Q64FUI;
DT 25-OCT-2004, integrated into UniProtKB/TREMBL.
DT 25-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.

```
DE Interleukin 23 p19 subunit.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=16293125;
RA Muilova P., Kubickova S., Vychodilova-Krenkova L., Kralik P.,
RA Matiasovic J., Hubertova D., Rubes J., Horin P.;
RT "Cytogenetic mapping of immunity-related genes in the domestic
RL horse.";
RL Anim. Genet. 36:507-510(2005).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY704416; AAU13947.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR010831; Cytokine_4_hlx.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR015947; IL23A; 1.
DR PANTHER; PTHR15947; IL23A; 1.
DR Pfam; PF00489; IL6; 1.
SQ SEQUENCE 192 AA; 21042 MW; 9898C79BC9E22E4F CRC64;

Query Match 87.0%; Score 873.5; DB 2; Length 192;
Best Local Similarity 88.0%; Pred. No. 2.5e-72;
Matches 169; Conservative 8; Mismatches 12; Indels 3; Gaps 2;

QY 1 MLGSRAVMLLLLPW--TAQGRAVPGSGSPAWTQCQQLSQKLCCTLAWSAHPLVGHMDL-R 57
DB 1 MLGSRAVMLLLLPWPTAQARAVPGSGSPAWACQQLSQKLCCTLAWSAHPVGHVDLP 60

QY 58 EBGDEETNDVPHIQCGDCDPOGLRDNQSFCLQRIHQGLIFVEKLGSDIFTGEPSSLP 117
DB 61 EBGDAETNDVPHIQCGDCDPEGLRDNQSPCLQRIHQGLVFEKLGSDIFTGEPSSLP 120

QY 118 DSPVAQLHASILGLSOLLQPEGHWHETQIIPSLSPSQPWQRLILRFLKILSLQAFAVAA 177
DB 121 NGPVDQLHASLGLURQLQPEGHWHETEIPSPSPSQPWQRLILRFLKILSLQAFAVAA 180

QY 178 RVFAHGAATLSP 189
DB 181 RVFAHGAATLTP 192

RESULT 6
ID Q9N2H9 PIG PRELIMINARY; PRT; 193 AA.
AC Q9N2H9;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DE 07-FEB-2006, entry version 12.
DR EMBL; AB030002; BAA93688.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR Sus scrofa (Pig).
DR Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hirata Y., Kosuge Y.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AB030002; BAA93688.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.

DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR010831; Cytokine_4_hlx.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; PTHR15947; IL23A; 1.
DR PANTHER; PTHR15947; IL23A; 1.
DR Pfam; PF00489; IL6; 1.
SQ SEQUENCE 189 AA; 20808 MW; BE06A3C59955337F CRC64;

Query Match 81.6%; Score 819; DB 2; Length 189;
Best Local Similarity 82.6%; Pred. No. 2.7e-67;
Matches 157; Conservative 12; Mismatches 19; Indels 2; Gaps 2;

QY 1 MLGSRAVMLLLLPWPTAQGRAVPGSGSPAWTQCQQLSQKLCCTLAWSAHPLVGHMDL-LREE 59
DB 1 MLGSTAVMLLLLPWPTAQGRAVPGSGSNPSTQCQQLSQKLCCTLAWSAHPVGHVPPREE 60

DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR010831; Cytokine_4_hlx.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; PTHR15947; IL23A; 1.
DR PANTHER; PTHR15947; IL23A; 1.
DR Pfam; PF00489; IL6; 1.
SQ SEQUENCE 193 AA; 21132 MW; 05F28DE94810B9E1 CRC64;

Query Match 84.3%; Score 846; DB 2; Length 193;
Best Local Similarity 85.4%; Pred. No. 8.8e-70;
Matches 164; Conservative 10; Mismatches 14; Indels 4; Gaps 2;

QY 1 MLGSRAVMM-----LLLLLPWTAQGRAVPGSGSPAWTQCQQLSQKLCCTLAWSAHPLVGHMDL- 56
DB 1 MLGSRAVMLMLLLLPWTSQGRAVPEGSSPAWAQQLSQQLCTLAHTAHLPMGHVDLP 60

QY 57 REEGDEETNDVPHIQCGDCDPOGLRDNQSFCLQRIHQGLIFVEKLGSDIFTGEPSSL 116
DB 61 REEGDDETTTSEVPHIQCGDCDPOGLRDNQSFCLQRIHQGLVFEKLGSDIFTGEPSSLH 120

QY 117 PDSFVAQLHASILGLSOLLQPEGHWHETQIIPSLSPSQPWQRLILRFLKILSLQAFAVAA 176
DB 121 PDGSGVQLHASILGLRLQLQPEGHWHETEPTSPSPSQPWQRLILRFLKILSLQAFAVAA 180

QY 177 ARVFAHGAATLS 188
DB 181 ARVFAHGAATLS 192

RESULT 7
ID Q6LA37 CAVPO PRELIMINARY; PRT; 189 AA.
AC Q6LA37;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DE 07-FEB-2006, entry version 8.
DR Interleukin-23 p19 subunit.
GN Names=IL-23 p19 subunit;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Hartley;
RA Shiratori I., Seya T.;
RT "Molecular cloning and functional characterization of guinea pig
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AB058509; BAD21123.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR010831; IL23A.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; PTHR15947; IL23A; 1.
DR Pfam; PF00489; IL6; 1.
SQ SEQUENCE 189 AA; 20808 MW; BE06A3C59955337F CRC64;

Query Match 81.6%; Score 819; DB 2; Length 189;
Best Local Similarity 82.6%; Pred. No. 2.7e-67;
Matches 157; Conservative 12; Mismatches 19; Indels 2; Gaps 2;

QY 1 MLGSRAVMLLLLPWPTAQGRAVPGSGSPAWTQCQQLSQKLCCTLAWSAHPLVGHMDL-LREE 59
DB 1 MLGSTAVMLLLLPWPTAQGRAVPGSGSNPSTQCQQLSQKLCCTLAWSAHPVGHVPPREE 60
```



```

RESULT 10
Q80WE2_PERMA PRELIMINARY; PRT; 184 AA.
AC Q80WE2;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Interleukin-23a subunit p19 (Fragment).
OS Peromyscus maniculatus (Deer mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Neotomidae; Peromyscus.
OX NCBI_TaxID=10042;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Schoutz T.;
RT "Cloning of deer mouse interleukin-23a p19 subunit."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY259629; AAP15041.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR010831; IL23A.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR PANTHER; PTHR15947; IL23A; 1.
DR Pfam; PF00489; IL6; 1.
FT NON TER 184
SQ SEQUENCE 184 AA; 20850 MW; 4045456CF6ACALC8 CRC64;

Query Match 76.5%; Score 768; DB 2; Length 184;
Best Local Similarity 78.7%; Pred. No. 1.3e-62;
Matches 144; Conservative 11; Mismatches 28; Indels 0; Gaps 0;

QY 1 MLCGRAVIMLLLPWTAGRAVPGSSPANTQCQQLSOKLCTLAWSAHLVGHMDLREEG 60
DB 1 MLCRAILLWLLPWTAGRAVPGSSPANTQCQQLSOKLCTLAWSAHLVGHMDLREEG 60
QY 61 DEETNDVPHIQCGDCDPQGLRDNSQFCLQRIHQGLIFYEKLIGSDIFTGEPSSLDPSP 120
DB 61 DEETNDVPHIQCGDCDPQGLRDNSQFCLQRIHQGLIFYEKLIGSDIFTGEPSSLDPSP 120
QY 121 VAQLHASLLGLSQQLQPEGHWHWETOQIPSLSPSQPWQRLRLKILRSLOAFVAARVF 180
DB 121 VGLHTSLGLSQQLQPEDRHWESEQMPSLRPSQWQRLRLKILRSLOAFVAARVF 180
QY 181 AHG 183
DB 181 AHG 183

RESULT 11
Q9EQ14_MOUSE PRELIMINARY; PRT; 196 AA.
AC Q9EQ14;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Interleukin 23 p19 subunit (interleukin 23, alpha subunit p19).
GN Name=IL23a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.

```

```

MEDLINE=20567322; PubMed=11114383; DOI=10.1016/S1074-7613(00)00070-4;
Oppmann B., Lesley R., Blom B., Timans J.C., Xu Y., Hunte B., Vega F.,
Yu N., Wang J., Singh K., Zonin F., Vaisberg E., Churakova T.,
Liu M.-R., Gorman D., Wagner J., Zurawski S., Liu Y.-J., Abrams J.S.,
Moore K.W., Rennick D., de Waal-Malefyt R., Hannum C., Bazan J.F.,
Kastelein R.A.;
RT "Novel p19 protein engages IL-12p40 to form a cytokine, IL-23, with
RT biological activities similar as well as distinct from IL-12."
RL Immunology 13:715-725(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Scherich A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RG NIH MGC Project;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF301619; AAG37231.1; -; mRNA.
DR EMBL; BC019953; AAH19953.1; -; mRNA.
DR Ensemble; ENSMUSG0000025383; Mus musculus.
DR MGI; MGI:1932410; IL23a.
DR GO; GO:0005615; C:extracellular space; RCA.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR010831; IL23A.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR PANTHER; PTHR15947; IL23A; 1.
DR Pfam; PF00489; IL6; 1.
DR ProDom; PD004356; Interleukin_6; 1.
DR SEQUENCE 196 AA; 22071 MW; DAF4A318A2DD3B7C CRC64;

Query Match 71.6%; Score 718.5; DB 2; Length 196;
Best Local Similarity 74.6%; Pred. No. 5.3e-58;
Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;

QY 1 MLCGRAVIMLLLPWTAGRAVPGSSPANTQCQQLSOKLCTLAWSAHLVGHMDLREE 59
DB 1 MLCRAVIMLLPWTAGRAVPGSSPANTQCQQLSOKLCTLAWSAHLVGHMDLREE 60
QY 60 GDEETNDVPHIQCGDCDPQGLRDNSQFCLQRIHQGLIFYEKLIGSDIFTGEPSSLPDS 119
DB 61 EDEETKNNVPRIQCEDGCDPQGLKDNSQFCLQRIHQGLIFYEKLIGSDIFTGEPSSLPDS 120
QY 120 PVAQLHASLLGLSQQLQPEGHWHWETOQIPSLSPSQPWQRLRLKILRSLOAFVAARV 179
DB 121 PMEQLHTSLGLSQQLQPEQHPRETQMPSPSSSQWQRLRLKILRSLOAFVAARV 180
QY 180 FAHGATLS 188

```

```
Db 181 FAHGATLT 189
|||||
RESULT 12
Q516V9 ENTHI PRELIMINARY; PRT; 236 AA.
AC Q516V9
DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 07-JUN-2006, sequence version 1.
DE Hypothetical protein.
GN ORFNames=s8.t00019;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=294381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAINS=HM-1:IMSS;
RX PubMed=15729342; DOI=10.1038/nature03291;
RA Lofus B.J., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
RA Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
RA Hofer M., Bruchhaus I., Willhoest U., Bhattacharya A.,
RA Chillingworth T., Churcher C.M., Hance Z., Harris B., Harris D.,
RA Jagels K., Moule S., Mungall K.L., Ormond D., Squares R.,
RA Whitehead S., Quail M.A., Rabinowitz S., Norbertczak H., Price C.,
RA Wang Z., Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S.,
RA Lohia A., Foster P.G., Sichert-Ponten T., Weber C., Singh U.,
RA Mukherjee C., El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M.,
RA Barrell B.G., Fraser C.M., Hall N.;
RT "The genome of the protist parasite Entamoeba histolytica.";
RL Nature 433:865-868(2005).
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
DR EMBL; AAFB01000228; EAL48883.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 28574 MW; 84011B98C36AC47C CRC64;

Query Match 10.7%; Score 107; DB 2; Length 236;
Best Local Similarity 28.8%; Pred. No. 0.19;
Matches 32; Conservative 18; Mismatches 35; Indels 26; Gaps 6;

QY 55 DLREGEDETTNDVPHICQDGDQGLRDNDSQFCLQRTHOGLIFVEKLLGSDIFTGSPS 114
Db 17 EIKDKIKETVDINNSECSEYDPPD-----EEDHQNIIPKFLGDKKP----- 61

QY 115 LPLDSPVAQLHASLGL-LSQLQPEG---HHWE---TQQIPSLSPSPQW 157
Db 62 --PQNLVGRF-AELGWGMEQELKPNGVFALHDEFTGDDDFDXLPPVVPQW 109

RESULT 13
CSF3_PIG
ID CSF3_PIG STANDARD; PRT; 195 AA.
AC 002837; O19180;
DT 15-JUL-1998, integrated into UniProtKB/Swiss-Prot.
DT 30-MAY-2006, sequence version 2.
DT 07-FEB-2006, entry version 33.
DE Granulocyte colony-stimulating factor precursor (G-CSF).
GN Name=CSF3;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].

RX MEDLINE=97473532; PubMed=9332386; DOI=10.1016/S0378-1119(97)00284-9;
RA Kulmburg P., Radke M., Mezes B., Mertelesmann R., Rosenthal F.M.;
RT "Cloning and sequence analysis of the immediate promoter region and
RT cDNA of porcine granulocyte colony-stimulating factor.";
RL Gene 197:361-365(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA].
RC TISSUE=Liver;
RA Gloster S.E., Sandeman R.M., Strom A.D.G.;
RT "Cloning of a cDNA and gene encoding porcine granulocyte-colony
RT stimulating factor.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: Granulocyte/macrophage colony-stimulating factors are
CC cytokines that act in hematopoiesis by controlling the production,
CC differentiation, and function of 2 related white cell populations
CC of the blood, the granulocytes and the monocytes-macrophages. This
CC CSF induces granulocytes (By similarity).
CC -! SUBUNIT: Monomer.
CC -! SUBCELLULAR LOCATION: Secreted protein.
CC -! PTM: O-glycosylated (By similarity).
CC -! SIMILARITY: Belongs to the IL-6 superfamily.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
DR EMBL; Y10494; CAA71518.1; -; mRNA.
DR EMBL; U68482; AAB70701.1; -; Genomic_DNA.
DR EMBL; U68481; AAB70700.1; -; mRNA.
DR HSSP; P09919; 1RHG.
DR SMR; Q02837; 26-195.
DR InterPro; IPR0012351; Cytokine_4_hlx.
DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 195
FT CARBOHYD 154 154
FT DISULFID 57 63 By similarity.
FT DISULFID 85 95 By similarity.
FT CONFLICT 123 123 A -> R (in Ref. 1).
SQ SEQUENCE 195 AA; 21214 MW; 84787F20DB0AEALC CRC64;

Query Match 10.6%; Score 106.5; DB 1; Length 195;
Best Local Similarity 24.9%; Pred. No. 0.17;
Matches 52; Conservative 28; Mismatches 76; Indels 53; Gaps 10;

QY 7 VMLLLLPTAGRAVPGGS--SPAWTQC-----OLSKQLCTLAWS 46
Db 3 LMAQLLLWHIALWVPEAPLSPASSLPQSFLLKLEQVRKIQADGAELQERLCATHKL 62

QY 47 AHP-----LVGHMDLREEGEDETTNDVPHICQDGDQGLRDNDSQFCLQRTHOGLIFVEK 102
Db 63 CHPQELVLLGH-----SLGLPQASL-SSCSQALQLTG--CLNQLHGGGLVYGG 108

QY 103 LLGSDIFTG-EPSLLPDSFVAQLHASLGLSOLLQPEGHWHWTQIQPSLSPSQ----- 154
Db 109 LL--QALAGISFELAPALDIQLQDVTDLATNIWLQME----DLRWAPASLFTQGTVPFT 162

QY 155 -PWQRLLRFKILRSLSQAFVAVARFAH 182
Db 163 SAFQRAGGVLVWSQLQSFLAYRVLRY 191

RESULT 14
Q8N4W3 HUMAN PRELIMINARY; PRT; 200 AA.
ID Q8N4W3 HUMAN
AC Q8N4W3;
```

```
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 21-FEB-2006, entry version 20.
DE Colony stimulating factor 3, isoform c.
GN Name=CSF3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S., Krzywinski M.I., Skalek U., Smallus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RA Straubeberg R.;
RA Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BC033245; AAF33245.1; -; mRNA.
DR HSSP; P09919; 1GNC.
DR SMR; Q8N4W3; 30-200.
DR Ensembl; ENSG00000108342; Homo sapiens.
DR GO; GO:0005615; C:extracellular space; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN6.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR NON TER 204 204
FT SEQUENCE 200 AA; 21543 MW; 8648AA55B329A96C CRC64;
SQ
Query Match 10.2%; Score 102; DB 2; Length 200;
Best Local Similarity 26.7%; Pred. No. 0.45; Indels 52; Gaps 12;
Matches 56; Conservative 21; Mismatches 81;
QY 4 SRVAMLL--LLPWTAGRAVPGSSPAWTQ-----CQQ-----LSQKLCITLAW 45
DQ 8 SPALQLLWHSALVTQ--EATPLGPASSLPQSFLKLCLEQVRKIQGDGAALQEKLCATYK 66
QY 46 SAHP-----LVGHMDLREGDEETNDVPHIQCGDGDGDPQGLRDNSQFCLORIHQGLIFYE 101
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 21-FEB-2006, entry version 20.
DE Colony stimulating factor 3, isoform c.
GN Name=CSF3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S., Krzywinski M.I., Skalek U., Smallus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RA Straubeberg R.;
RA Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BC033245; AAF33245.1; -; mRNA.
DR HSSP; P09919; 1GNC.
DR SMR; Q8N4W3; 30-200.
DR Ensembl; ENSG00000108342; Homo sapiens.
DR GO; GO:0005615; C:extracellular space; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN6.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR NON TER 204 204
FT SEQUENCE 200 AA; 21543 MW; 8648AA55B329A96C CRC64;
SQ
Query Match 10.2%; Score 102; DB 2; Length 200;
Best Local Similarity 26.7%; Pred. No. 0.45; Indels 52; Gaps 12;
Matches 56; Conservative 21; Mismatches 81;
QY 4 SRVAMLL--LLPWTAGRAVPGSSPAWTQ-----CQQ-----LSQKLCITLAW 45
DQ 8 SPALQLLWHSALVTQ--EATPLGPASSLPQSFLKLCLEQVRKIQGDGAALQEKLCATYK 66
QY 46 SAHP-----LVGHMDLREGDEETNDVPHIQCGDGDGDPQGLRDNSQFCLORIHQGLIFYE 101
Db 15 WTAGRAVPGSSPAWTQ-----CQQ-----LSQKLCITLAWSAHP-----LVGHM 54
DQ 25 WTQV--EATPLGPASSLPQSFLKLCLEQVRKIQGDGAALQEKLCATYKCLPEELVLGH- 82
QY 55 DLREGDEETNDVPHIQCGDGDGDPQGLRDNSQFCLORIHQGLIFYEKLGSDIFTG-EP 113
DQ 83 -----SLGIPWAPL--SSCFPSQALQ--LAGCLSQLHSLGLFYQGLL--QALEGISP 127
QY 114 SLPLSPDPAQLHASLGLSQLLPQEGHHWETQIIPSLSPSQ-----PQRLLLLFKI 165
DQ 128 ELGPTLDTLQLDVADFATTIQQME-----ELGMAPALQPTQGAMPAPAFORRGVLV 183
QY 166 LRSIQAFVAARVFAH 182
DQ 184 ASHLQSFLEVSRYLRH 200
```

Search completed: June 20, 2006, 04:39:26
Job time : 215.627 secs

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2006, 04:40:29 ; Search time 35.8364 Seconds
(without alignments)
461.634 Million cell updates/sec

Title: US-10-797-157-2
Perfect score: 1004
Sequence: 1 MLGSRVNMVLLPWTQAQR.....QAFVAVARVFAHGAATLSP 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5 COMB.psp:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6 COMB.psp:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7 COMB.psp:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H COMB.psp:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCRUS COMB.psp:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE COMB.psp:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.psp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1004	100.0	189	2	US-09-122-443-2 Sequence 2, Appli
2	1004	100.0	189	2	US-09-558-089-2 Sequence 2, Appli
3	1004	100.0	189	2	US-09-558-087-2 Sequence 2, Appli
4	1004	100.0	189	2	US-09-558-474-2 Sequence 2, Appli
5	1004	100.0	189	6	US-09-935-366A-2 Sequence 2, Appli
6	1000	99.6	189	2	US-09-687-637B-1 Sequence 1, Appli
7	718.5	71.6	196	2	US-09-122-443-4 Sequence 4, Appli
8	718.5	71.6	196	2	US-09-558-089-4 Sequence 4, Appli
9	718.5	71.6	196	2	US-09-558-087-4 Sequence 4, Appli
10	718.5	71.6	196	2	US-09-558-474-4 Sequence 4, Appli
11	718.5	71.6	196	6	US-09-935-366A-4 Sequence 4, Appli
12	463	46.1	102	2	US-09-122-443-5 Sequence 5, Appli
13	463	46.1	102	2	US-09-558-089-5 Sequence 5, Appli
14	463	46.1	102	2	US-09-558-087-5 Sequence 5, Appli
15	463	46.1	102	2	US-09-558-474-5 Sequence 5, Appli
16	463	46.1	102	6	US-09-935-366A-5 Sequence 5, Appli
17	291	29.0	54	2	US-09-687-637B-22 Sequence 22, Appli
18	277	27.6	53	2	US-09-687-637B-25 Sequence 25, Appli
19	245	24.4	49	2	US-09-687-637B-24 Sequence 24, Appli
20	187	18.6	33	2	US-09-687-637B-23 Sequence 23, Appli
21	107	10.7	175	2	US-09-479-313B-13 Sequence 13, Appli
22	105	10.5	175	2	US-09-479-313B-12 Sequence 12, Appli
23	103	10.3	175	2	US-09-479-313B-9 Sequence 9, Appli
24	103	10.3	175	2	US-09-479-313B-14 Sequence 14, Appli
25	102	10.2	174	2	US-09-950-123-4 Sequence 4, Appli
26	102	10.2	175	2	US-09-479-313B-7 Sequence 7, Appli

27	102	10.2	307	2	US-08-469-318-121	Sequence 121, App
28	102	10.2	307	2	US-08-469-318-122	Sequence 122, App
29	102	10.2	307	2	US-08-469-318-134	Sequence 134, App
30	102	10.2	307	2	US-08-469-318-135	Sequence 135, App
31	102	10.2	307	2	US-08-468-609A-121	Sequence 121, App
32	102	10.2	307	2	US-08-468-609A-122	Sequence 122, App
33	102	10.2	307	2	US-08-468-609A-134	Sequence 134, App
34	102	10.2	307	2	US-08-468-609A-135	Sequence 135, App
35	102	10.2	307	2	US-08-446-872A-121	Sequence 121, App
36	102	10.2	307	2	US-08-446-872A-122	Sequence 122, App
37	102	10.2	307	2	US-08-446-872A-134	Sequence 134, App
38	102	10.2	307	2	US-08-446-872A-135	Sequence 135, App
39	102	10.2	307	2	US-08-762-227A-121	Sequence 121, App
40	102	10.2	307	2	US-08-762-227A-122	Sequence 122, App
41	102	10.2	307	2	US-08-762-227A-134	Sequence 134, App
42	102	10.2	307	2	US-08-762-227A-135	Sequence 135, App
43	102	10.2	307	5	PCT-US95-01185-121	Sequence 121, App
44	102	10.2	307	5	PCT-US95-01185-122	Sequence 122, App
45	102	10.2	307	5	PCT-US95-01185-134	Sequence 134, App

ALIGNMENTS

RESULT 1
US-09-122-443-2
; Sequence 2, Application US/09122443
; Patent No. 6060284
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/122,443
; FILING DATE: 24-JUL-1998
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,765
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 189 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-122-443-2

Query Match 100.0%; Score 1004; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 1.6e-106;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLGSRVNMVLLPWTQAQRVPGSSPAWTCQQLSOKLCTLAWSAHLVGHMDLREG 60
Db 1 MLGSRVNMVLLPWTQAQRVPGSSPAWTCQQLSOKLCTLAWSAHLVGHMDLREG 60

Qy	61	DEETNDVPHICGGDCDPOGLRDNQPCLORIHQGLIFYEKLIGSDIFTGEPSLLPDSF	120
Db	61	DEETNDVPHICGGDCDPOGLRDNQPCLORIHQGLIFYEKLIGSDIFTGEPSLLPDSF	120
Qy	121	VQLQHASLLGLSQLQPEGHHWETQOIPSLSPSPQWRLLLRKFILRSLOAFVAAVAAF	180
Db	121	VQLQHASLLGLSQLQPEGHHWETQOIPSLSPSPQWRLLLRKFILRSLOAFVAAVAAF	180
Qy	181	AHGAATLSP	189
Db	181	AHGAATLSP	189

RESULT 2
US-09-558-089-2
; Sequence 2, Application US/09558089
; Patent No. 6479634
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN
CYTOKINE: RELATED REAGENTS

Qy 181 AHGAATLSP 189
 |||||
 Db 181 AHGAATLSP 189

RESULT 3
 US-09-558-087-2
 ; Sequence 2, Application US/09558087
 ; Patent No. 6495667
 ; GENERAL INFORMATION:
 ; APPLICANT: Bazan, J. Fernando
 ; TITLE OF INVENTION: MAMMALIAN
 ; CYTOKINE; RELATED REAGENTS

ADDRESSEE: DNAX Research
STREET: 901 California
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104

GENERAL INFORMATION:
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA

ZIB: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/558.474
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION NUMBER: US 60/053,765
APPLICATION NUMBER: 08/000,000
FILING DATE: 23-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Chiang, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0758K1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-9196
TELEFAX: (650) 496-1200

Query Match	100.0%;	Score 1004;	DB 2;	Length 189;
Best Local Similarity	100.0%;	Pred. No. 1.6e-106;		
Matches 189;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MLGSRAVMLLLLLPWTAAQGRAVPGGSSPANTQCQOLSKQLCTLAWSAHPLVGHMDLREEG	60	
DB	1	MLGSRAVMLLLLLPWTAAQGRAVPGGSSPANTQCQOLSKQLCTLAWSAHPLVGHMDLREEG	60	
QY	61	DEETNDVPHIQCGDGCDDPGLRDNQFCQLRHHQGLIFYEKLGLSDIFTEGPSLLDPSP	120	
DB	61	DEETNDVPHIQCGDGCDDPGLRDNQFCQLRHHQGLIFYEKLGLSDIFTEGPSLLDPSP	120	
QY	121	VAQHLASLLGLSOLLQPEGHHWETQQIPSLSPSPQWQRLRLRFLKILRSLOAFVAVAAVRF	180	
DB	121	VAQHLASLLGLSOLLQPEGHHWETQQIPSLSPSPQWQRLRLRFLKILRSLOAFVAVAAVRF	180	
QY	181	AHGAATLSP	189	
DB	181	AHGAATLSP	189	

RESULT 5
US-09-935-366A-2
; Sequence 2, Application US/09935366A
; Patent No. RE39015
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California

COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/935,366A
FILING DATE: 22-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/122,443
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0758K1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
PS-09-935-166A-2

	Query Match	100.0%;	Score 1004;	DB 6;	Length 189;
	Best Local Similarity	100.0%;	Pred. No. 1.6e-106;		
	Matches 189;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MLGSRAVMLLLLPWTAQGRAVPGSGSSPAWTCQOQLSOKLCTLAWSAHPLVGHMDLREEG	60		
Db	1	MLGSRAVMLLLLPWTAQGRAVPGSGSSPAWTCQOQLSOKLCTLAWSAHPLVGHMDLREEG	60		
Qy	61	DEETNDVPHIQCGDGDGPGLRDNSQFCQLRTHOGLIFYEKLLGSDIFTGEPSLLPDSP	120		
Db	61	DEETNDVPHIQCGDGDGPGLRDNSQFCQLRTHOGLIFYEKLLGSDIFTGEPSLLPDSP	120		
Qy	121	VAQHASLGLSOLLQPEGHHWETQIQPSLSPSQPWQRLLRPFKILRSLQAFVAVAARVF	180		
Db	121	VAQHASLGLSOLLQPEGHHWETQIQPSLSPSQPWQRLLRPFKILRSLQAFVAVAARVF	180		
Qy	181	AHGAATLSP	189		
Db	181	AHGAATLSP	189		

```

RESULT 6
US-09-687-637B-1
; Sequence 1, Application US/09687637B
; Patent No. 6610285
; GENERAL INFORMATION:
; APPLICANT: Hirata, Yuichi
; TITLE OF INVENTION: CYTOKINE-LIKE PROTEINS THAT PROMOTE CELL PROLIFERATION
; FILE REFERENCE: 06501-067001
; CURRENT APPLICATION NUMBER: US/09/687,637B
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: PCT/JP99/01997
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: JP 10/121805
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-687-637B-1

```


RESULT 9
US-09-558-087-4

; Sequence 4, Application US/09558087
; Patent No. 6495667
; GENERAL INFORMATION:

APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESS: DNAX Research Institute

STREET: 901 California Avenue

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/558,087

FILING DATE: 25-Apr-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/053,765

FILING DATE: 25-JUL-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: DX0758K1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650)852-9196

TELEFAX: (650)496-1200

SEQUENCE CHARACTERISTICS:

LENGTH: 196 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-558-087-4

Query Match 71.6%; Score 718.5; DB 2; Length 196;

Best Local Similarity 74.6%; Pred. No. 7.3e-74;

Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;

QY 1 MLGSAVMLLLPWTAGRAVPGSSPAWTCQQLSOKLCTLAWSAHPLVGHMD-LREE 59

Db 1 MLDCAVIMLLPWTQGLAVPRSSPDWACQQLSRNLCMLAWNAHAPAGHMLLREE 60

QY 60 GDEETNDVPHIQCGDGDGCDPQGLRDNQSFCLOIRHQGLIFYEKLGLSDIFTGPEPSLLPDS 119

Db 61 EDEETKNVPRIQCGDGDGCDPQGLKNSQFCLOIRQGLAFYKHLSDIFKGEPAALLPDS 120

QY 120 PVAQLHASLLGLSLLQPEGHHWETQIIPSLSPSPQWOLLRFKILRSLOAFVAARV 179

Db 121 PMEQLTSLGLSLLQPEGHHWETQIIPSLSPSPQWOLLRFKILRSLOAFVAARV 180

QY 180 FAHGAATLS 188

Db 181 FAHGAATLT 189

RESULT 10

US-09-558-474-4

; Sequence 4, Application US/09558474

; Patent No. 6835825

; GENERAL INFORMATION:

APPLICANT: Bazan, J. Fernando

TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS

NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:

ADDRESS: DNAX Research Institute

STREET: 901 California Avenue

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/558,474

FILING DATE: 25-Apr-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/053,765

FILING DATE: 25-JUL-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: DX0758K1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650)852-9196

TELEFAX: (650)496-1200

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 196 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-558-474-4

Query Match

Best Local Similarity 71.6%; Score 718.5; DB 2; Length 196;

Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;

QY 1 MLGSAVMLLLPWTAGRAVPGSSPAWTCQQLSOKLCTLAWSAHPLVGHMD-LREE 59

Db 1 MLDCAVIMLLPWTQGLAVPRSSPDWACQQLSRNLCMLAWNAHAPAGHMLLREE 60

QY 60 GDEETNDVPHIQCGDGDGCDPQGLRDNQSFCLOIRHQGLIFYEKLGLSDIFTGPEPSLLPDS 119

Db 61 EDEETKNVPRIQCGDGDGCDPQGLKNSQFCLOIRQGLAFYKHLSDIFKGEPAALLPDS 120

QY 120 PVAQLHASLLGLSLLQPEGHHWETQIIPSLSPSPQWOLLRFKILRSLOAFVAARV 179

Db 121 PMEQLTSLGLSLLQPEGHHWETQIIPSLSPSPQWOLLRFKILRSLOAFVAARV 180

QY 180 FAHGAATLS 188

Db 181 FAHGAATLT 189

RESULT 11

US-09-935-366A-4

; Sequence 4, Application US/09935366A

; Patent No. R839015

; GENERAL INFORMATION:

APPLICANT: Bazan, J. Fernando

TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESS: DNAX Research Institute

STREET: 901 California Avenue

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1104

COMPUTER READABLE FORM:

```
;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/935,366A
; FILING DATE: 22-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/122,443
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 196 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-935-366A--4

Query Match 71.6%; Score 718.5; DB 6; Length 196;
Best Local Similarity 74.6%; Pred. No. 7.3e-74;
Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;

Qy 1 MLGSRVMLLLPWTAGRAVPGSSPAWTCQQLSQKLCCTLAWSAHLVGHMD-LREE 59
Db 1 MLDCAVIMLWLLPWVQGLAVPRSSPDWAQCCQLSRNLCMLAWNAHAPAGHNNLLREE 60

Qy 60 GDETTNDVPHIQCGDCGDPGLRDNQFCLQRHQGLFYFKLIGSDIFTGEPSSLPDS 119
Db 61 EDETKNNVRIQEDCGDCPGLRDNQFCLQRHQGLFYFKLIGSDIFTGEPSSLPDS 120

Qy 120 PVAQLHASLGLSLLQLOPEGHWHWTQIPSLSPQWQRLRLRPFKILRSLOAFVAVARV 179
Db 121 PMEQLHSLGLSLLQLOPEGHWHWTQIPSLSPQWQRLRLRPFKILRSLOAFVAVARV 180

Qy 180 FAHGAATLS 188
Db 181 FAHGAATLT 189

RESULT 12
US-09-122-443-5
; Sequence 5, Application US/09122443
; Patent No. 6060284
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/122,443
; FILING DATE: 24-JUL-1998
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/558,089
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/122,443
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

; APPLICATION NUMBER: US 60/053,765
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-122-443-5

Query Match 46.1%; Score 463; DB 2; Length 102;
Best Local Similarity 90.0%; Pred. No. 4.7e-45;
Matches 90; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 89 CLQRIHQGLIFYEKLIGSDIFTGEPSSLPDS PVAQLHASLGLSLLQLOPEGHWHWTQIP 148
Db 2 CLQRIHQGLIFYEKLIGSDIFTGEPSSLPDS PVAQLHASLGLSLLQLOPEGHWHWTQIP 61

Qy 149 SLSPSQWQRLRLRPFKILRSLOAFVAVARVFAHGAATLS 188
Db 62 SPSPSQWQRLRLRPFKILRSLOAFVAVARVFAHGAATLS 101

RESULT 13
US-09-558-089-5
; Sequence 5, Application US/09558089
; Patent No. 6479634
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/558,089
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/122,443
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
```

US-09-558-089-5

Query Match 46.1%; Score 463; DB 2; Length 102;
Best Local Similarity 90.0%; Pred. No. 4.7e-45;
Matches 90; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
QY 89 CLQRHQGLIFVEKLGSDIFTGPESLPDSPVAQLHASLLGLSLLQLQPEGHHWETQIP 148
Db 2 CLQRHQGLVFEKLGSDIFTGPESLHPDGSVGLHSLGLRLQLQPEGHHWETQIP 61
QY 149 SLSPSQPWORLLRLKILRSLOAFVAVARVFAHGAATLS 188
Db 62 SPSPSQPWORLLRLKILRSLOAFVAVARVFAHGAATLS 101

RESULT 14

US-09-558-087-5
; Sequence 5, Application US/09558087
; Patent No. 6495667
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/558,087
; FILING DATE: 25-APR-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,765
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 852-9196
; TELEFAX: (650) 496-1200
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-558-087-5

Query Match 46.1%; Score 463; DB 2; Length 102;
Best Local Similarity 90.0%; Pred. No. 4.7e-45;
Matches 90; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
QY 89 CLQRHQGLIFVEKLGSDIFTGPESLPDSPVAQLHASLLGLSLLQLQPEGHHWETQIP 148
Db 2 CLQRHQGLVFEKLGSDIFTGPESLHPDGSVGLHSLGLRLQLQPEGHHWETQIP 61
QY 149 SLSPSQPWORLLRLKILRSLOAFVAVARVFAHGAATLS 188
Db 62 SPSPSQPWORLLRLKILRSLOAFVAVARVFAHGAATLS 101

RESULT 15

US-09-558-474-5

; Sequence 5, Application US/09558474
; Patent No. 6835825
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/558,474
; FILING DATE: 25-APR-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,765
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 852-9196
; TELEFAX: (650) 496-1200
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-558-474-5
Query Match 46.1%; Score 463; DB 2; Length 102;
Best Local Similarity 90.0%; Pred. No. 4.7e-45;
Matches 90; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
QY 89 CLQRHQGLIFVEKLGSDIFTGPESLPDSPVAQLHASLLGLSLLQLQPEGHHWETQIP 148
Db 2 CLQRHQGLVFEKLGSDIFTGPESLHPDGSVGLHSLGLRLQLQPEGHHWETQIP 61
QY 149 SLSPSQPWORLLRLKILRSLOAFVAVARVFAHGAATLS 188
Db 62 SPSPSQPWORLLRLKILRSLOAFVAVARVFAHGAATLS 101
Search completed: June 20, 2006, 04:41:50
Job time : 36.8364 secs

THIS PAGE BLANK (USP 12)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2006, 04:40:39 ; Search time 138.436 seconds
(without alignments)
632.403 Million cell updates/sec

Title: US-10-797-157-2

Perfect score: 1004

Sequence: 1 MLGSRVNMVLLPWTAGQR.....QAFVAVAAVFAGGAATLSP 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /EMC_Celerra_IDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_IDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_IDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_IDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_IDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_IDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1004	100.0	189	4	US-10-375-706-2 Sequence 2, Appli
2	1004	100.0	189	4	US-10-742-405-4 Sequence 4, Appli
3	1004	100.0	189	5	US-10-797-157-2 Sequence 2, Appli
4	1004	100.0	189	5	US-10-720-026-6 Sequence 6, Appli
5	1004	100.0	189	6	US-11-006-154-2 Sequence 2, Appli
6	1000	99.6	189	3	US-09-965-528-14 Sequence 14, Appl
7	1000	99.6	189	3	US-09-374-046A-138 Sequence 138, App
8	1000	99.6	189	3	US-09-969-984-14 Sequence 14, Appl
9	1000	99.6	189	4	US-10-028-072-232 Sequence 232, App
10	1000	99.6	189	4	US-10-140-808-232 Sequence 232, App
11	1000	98.6	189	4	US-10-121-049-232 Sequence 232, App
12	1000	99.6	189	4	US-10-123-904-232 Sequence 232, App
13	1000	99.6	189	4	US-10-140-470-232 Sequence 232, App
14	1000	99.6	189	4	US-10-175-746-232 Sequence 232, App
15	1000	99.6	189	4	US-10-176-918-232 Sequence 232, App
16	1000	99.6	189	4	US-10-176-921-232 Sequence 232, App
17	1000	98.6	189	4	US-10-137-865-232 Sequence 232, App
18	1000	99.6	189	4	US-10-140-474-232 Sequence 232, App
19	1000	99.6	189	4	US-10-142-431-232 Sequence 232, App
20	1000	99.6	189	4	US-10-143-114-232 Sequence 232, App
21	1000	99.6	189	4	US-10-142-419-232 Sequence 232, App
22	1000	99.6	189	4	US-10-123-262-232 Sequence 232, App
23	1000	98.6	189	4	US-10-142-423-232 Sequence 232, App
24	1000	99.6	189	4	US-10-121-050-232 Sequence 232, App
25	1000	99.6	189	4	US-10-141-755-232 Sequence 232, App
26	1000	99.6	189	4	US-10-143-032-232 Sequence 232, App
27	1000	99.6	189	4	US-10-123-108-232 Sequence 232, App

ALIGNMENTS

RESULT 1

US-10-375-706-2
; Sequence 2, Application US/10375706
; Publication No. US20030162261A1
; GENERAL INFORMATION:
; APPLICANT: De Waal Malefyt, Rene
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Lira, Sergio A.
; APPLICANT: Narula, Satwant
; APPLICANT: Oppmann, Birgit
; APPLICANT: Remnick, Donna M.
; APPLICANT: Wiekowski, Maria
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
; FILE REFERENCE: DX01042X US
; CURRENT APPLICATION NUMBER: US/10/375,706
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US/09/658,699
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 09/393,090
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 60/164,616
; PRIOR FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: surmised Homo sapiens
US-10-375-706-2

Query Match 100.0%; Score 1004; DB 4; Length 189;

Best Local Similarity 100.0%; Pred. No. 1.7e-95;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MLGSRVNMVLLPWTAGQRAVPGGSSPAWTCQQLSQKLCITLAWSAHPLVGHMDLREEG	60
DB	1	MLGSRVNMVLLPWTAGQRAVPGGSSPAWTCQQLSQKLCITLAWSAHPLVGHMDLREEG	60
QY	61	DEETNDVPHIQCGDCDPQGLRDNSQCLQRIHQGLIFYEKLIGSDIFTGSPSLPDSP	120
DB	61	DEETNDVPHIQCGDCDPQGLRDNSQCLQRIHQGLIFYEKLIGSDIFTGSPSLPDSP	120
QY	121	VAQLHASLGLSOLLQPEGHWHWETQIPLSPSPQWQRLLRFKILRSIQAFVAAVAVF	180
DB	121	VAQLHASLGLSOLLQPEGHWHWETQIPLSPSPQWQRLLRFKILRSIQAFVAAVAVF	180
QY	181	AHGAATLSP	189

```
Db      181 AHGAATLSP 189
|||||
RESULT 2
US-10-742-405-4
; Sequence 4, Application US/10742405
; Publication No. US20040213761A1
; GENERAL INFORMATION:
; APPLICANT: Bowman, Edward P.
; APPLICANT: Chan, Jason R.
; APPLICANT: Moore, Kevin
; APPLICANT: Nguyen, Nhung
; APPLICANT: Churakova, Tatyana
; APPLICANT: Chen, Shi-Juan
; APPLICANT: Cua, Daniel J.
; TITLE OF INVENTION: Uses of mammalian cytokine; related reagents
; FILE REFERENCE: DX01578K
; CURRENT APPLICATION NUMBER: US/10/742,405
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-742-405-4

Query Match      100.0%; Score 1004; DB 4; Length 189;
Best Local Similarity 100.0%; Pred. No. 1.7e-95;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MLGSRAVMLLLLPWTAQGRAVPGSSPAWTCQQLSQKLTLSAHPVGHMDLREEG 60
Db      1 MLGSRAVMLLLLPWTAQGRAVPGSSPAWTCQQLSQKLTLSAHPVGHMDLREEG 60

Qy      61 DEETTNDVPHIQCGDCDPQGLRDNSQFCLQRHQGLIFYEKLGSDIFTGEPSSLDPSP 120
Db      61 DEETTNDVPHIQCGDCDPQGLRDNSQFCLQRHQGLIFYEKLGSDIFTGEPSSLDPSP 120

Qy      121 VAQLHASLLGLSOLLQPEGHWHWETQIIPSLSPSPQWQRLRLRPFKILRSLOAFVAVAARVF 180
Db      121 VAQLHASLLGLSOLLQPEGHWHWETQIIPSLSPSPQWQRLRLRPFKILRSLOAFVAVAARVF 180

Qy      181 AHGAATLSP 189
Db      181 AHGAATLSP 189

RESULT 3
US-10-797-157-2
; Sequence 2, Application US/10797157
; Publication No. US20040223969A1
; GENERAL INFORMATION:
; APPLICANT: Oft, Martin
; APPLICANT: McClanahan, Terrill K.
; TITLE OF INVENTION: USES OF IL-23 AGONISTS AND ANTAGONISTS; RELATED REAGENTS
; FILE REFERENCE: DX06022US01
; CURRENT APPLICATION NUMBER: US/10/797,157
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: U.S. 60/453,672
; PRIOR FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-797-157-2

Query Match      100.0%; Score 1004; DB 5; Length 189;
Best Local Similarity 100.0%; Pred. No. 1.7e-95;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MLGSRAVMLLLLPWTAQGRAVPGSSPAWTCQQLSQKLTLSAHPVGHMDLREEG 60
Db      1 MLGSRAVMLLLLPWTAQGRAVPGSSPAWTCQQLSQKLTLSAHPVGHMDLREEG 60

Qy      61 DEETTNDVPHIQCGDCDPQGLRDNSQFCLQRHQGLIFYEKLGSDIFTGEPSSLDPSP 120
Db      61 DEETTNDVPHIQCGDCDPQGLRDNSQFCLQRHQGLIFYEKLGSDIFTGEPSSLDPSP 120

Qy      121 VAQLHASLLGLSOLLQPEGHWHWETQIIPSLSPSPQWQRLRLRPFKILRSLOAFVAVAARVF 180
Db      121 VAQLHASLLGLSOLLQPEGHWHWETQIIPSLSPSPQWQRLRLRPFKILRSLOAFVAVAARVF 180

Qy      181 AHGAATLSP 189
Db      181 AHGAATLSP 189

RESULT 4
US-10-720-026-6
; Sequence 6, Application US/10720026
; Publication No. US20040258686A1
; GENERAL INFORMATION:
; APPLICANT: Chirica, Madeline
; APPLICANT: Parham, Christi L.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Moore, Kevin W.
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.
; FILE REFERENCE: DX01074B1K
; CURRENT APPLICATION NUMBER: US/10/720,026
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: 60/203,426
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-720-026-6

Query Match      100.0%; Score 1004; DB 5; Length 189;
Best Local Similarity 100.0%; Pred. No. 1.7e-95;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MLGSRAVMLLLLPWTAQGRAVPGSSPAWTCQQLSQKLTLSAHPVGHMDLREEG 60
Db      1 MLGSRAVMLLLLPWTAQGRAVPGSSPAWTCQQLSQKLTLSAHPVGHMDLREEG 60

Qy      61 DEETTNDVPHIQCGDCDPQGLRDNSQFCLQRHQGLIFYEKLGSDIFTGEPSSLDPSP 120
Db      61 DEETTNDVPHIQCGDCDPQGLRDNSQFCLQRHQGLIFYEKLGSDIFTGEPSSLDPSP 120

Qy      121 VAQLHASLLGLSOLLQPEGHWHWETQIIPSLSPSPQWQRLRLRPFKILRSLOAFVAVAARVF 180
Db      121 VAQLHASLLGLSOLLQPEGHWHWETQIIPSLSPSPQWQRLRLRPFKILRSLOAFVAVAARVF 180

Qy      181 AHGAATLSP 189
Db      181 AHGAATLSP 189

RESULT 5
US-11-006-154-2
; Sequence 2, Application US/11006154
; Publication No. US20050158750A1
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
```


CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/11/006,154
FILING DATE: 06-Dec-2004
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
FILING DATE: 22-Aug-2001
APPLICATION NUMBER: 09/122,443
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0758K1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 189 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-11-006-154-2

Query Match 100.0%; Score 1004; DB 6; Length 189;
Best Local Similarity 100.0%; Pred. No. 1.7e-95;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLGSRVAMLLLLPWTAGRAVPGGSSPAWTCQQLSQKLTLSAHPVGHMDLREEG 60
DB 1 MLGSRVAMLLLLPWTAGRAVPGGSSPAWTCQQLSQKLTLSAHPVGHMDLREEG 60
QY 61 DEETNDVPHIQCGDGPQGLRDNQFCLQRIHQGLIFYEKLIGSDIFTGEPSSLDPSP 120
DB 61 DEETNDVPHIQCGDGPQGLRDNQFCLQRIHQGLIFYEKLIGSDIFTGEPSSLDPSP 120
QY 121 VAQLHASLLGLSQLLQPEGHWHWETQIIPSLSPSPQWQRLRLFKILRSLOAFVAVARVF 180
DB 121 VAQLHASLLGLSQLLQPEGHWHWETQIIPSLSPSPQWQRLRLFKILRSLOAFVAVARVF 180
QY 181 AHGAATLSP 189
DB 181 AHGAATLSP 189

RESULT 6
US-09-965-528-14
Sequence 14, Application US/09965528
Publication No. US20020187523A1
GENERAL INFORMATION:
APPLICANT: TANG, Y. Tom
APPLICANT: YUE, Henry
APPLICANT: LAL, Preeti
APPLICANT: BURFORD, Neil
APPLICANT: BANDMAN, Olga
APPLICANT: BAUGHN, Mariah R.
APPLICANT: AZIMZAI, Valda
APPLICANT: LU, Dying Aina M.
APPLICANT: PATTERSON, Chandra
TITLE OF INVENTION: EXTRACELLULAR SIGNALING MOLECULES
FILE REFERENCE: PF-0701 USA
CURRENT APPLICATION NUMBER: US/09/965,528

CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/134,949
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/144,270
PRIOR FILING DATE: 1999-07-15
PRIOR APPLICATION NUMBER: 60/146,700
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 60/157,508
PRIOR FILING DATE: 1999-10-04
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PERL Program
SEQ ID NO 14
LENGTH: 189
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No. US20020187523A1 2933038CD1
US-09-965-528-14

Query Match 99.6%; Score 1000; DB 3; Length 189;
Best Local Similarity 99.5%; Pred. No. 4.4e-95;
Matches 188; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLGSRVAMLLLLPWTAGRAVPGGSSPAWTCQQLSQKLTLSAHPVGHMDLREEG 60
DB 1 MLGSRVAMLLLLPWTAGRAVPGGSSPAWTCQQLSQKLTLSAHPVGHMDLREEG 60
QY 61 DEETNDVPHIQCGDGPQGLRDNQFCLQRIHQGLIFYEKLIGSDIFTGEPSSLDPSP 120
DB 61 DEETNDVPHIQCGDGPQGLRDNQFCLQRIHQGLIFYEKLIGSDIFTGEPSSLDPSP 120
QY 121 VAQLHASLLGLSQLLQPEGHWHWETQIIPSLSPSPQWQRLRLFKILRSLOAFVAVARVF 180
DB 121 VAQLHASLLGLSQLLQPEGHWHWETQIIPSLSPSPQWQRLRLFKILRSLOAFVAVARVF 180
QY 181 AHGAATLSP 189
DB 181 AHGAATLSP 189

RESULT 7
US-09-374-046A-138
Sequence 138, Application US/09374046A
Publication No. US20030096951A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Agostino, Michael J.
APPLICANT: Steiningger II, Robert J.
APPLICANT: Spaulding, Vikki
APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
APPLICANT: Fechtel, Kim
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: GI 6075-83A
CURRENT APPLICATION NUMBER: US/09/374,046A
CURRENT FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 138
LENGTH: 189
TYPE: PRT
ORGANISM: Homo sapiens
US-09-374-046A-138

Query Match 99.6%; Score 1000; DB 3; Length 189;

; PRIOR FILING DATE: 1997-10-29
 ; PRIOR APPLICATION NUMBER: 60/063733
 ; PRIOR FILING DATE: 1997-10-29
 ; PRIOR APPLICATION NUMBER: 60/063735
 ; PRIOR FILING DATE: 1997-10-29
 ; PRIOR APPLICATION NUMBER: 60/063738
 ; PRIOR FILING DATE: 1997-10-29
 ; PRIOR APPLICATION NUMBER: 60/063755
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/064248
 ; PRIOR FILING DATE: 1997-11-03
 ; PRIOR APPLICATION NUMBER: 60/064809
 ; PRIOR FILING DATE: 1997-11-07
 ; PRIOR APPLICATION NUMBER: 60/065186
 ; PRIOR FILING DATE: 1997-11-12
 ; PRIOR APPLICATION NUMBER: 60/065846
 ; PRIOR FILING DATE: 1997-11-17
 ; PRIOR APPLICATION NUMBER: 60/066364
 ; PRIOR FILING DATE: 1997-11-21
 ; PRIOR APPLICATION NUMBER: 60/066453
 ; PRIOR FILING DATE: 1997-11-24
 ; PRIOR APPLICATION NUMBER: 60/066511
 ; PRIOR FILING DATE: 1997-11-24
 ; PRIOR APPLICATION NUMBER: 60/066770
 ; PRIOR FILING DATE: 1997-11-24
 ; PRIOR APPLICATION NUMBER: 60/069212
 ; PRIOR FILING DATE: 1997-12-11
 ; PRIOR APPLICATION NUMBER: 60/069278
 ; PRIOR FILING DATE: 1997-12-11
 ; PRIOR APPLICATION NUMBER: 60/069334
 ; PRIOR FILING DATE: 1997-12-11
 ; PRIOR APPLICATION NUMBER: 60/069694
 ; PRIOR FILING DATE: 1997-12-16
 ; PRIOR APPLICATION NUMBER: 60/072320
 ; PRIOR FILING DATE: 1998-01-23
 ; PRIOR APPLICATION NUMBER: 60/073612
 ; PRIOR FILING DATE: 1998-02-04
 ; PRIOR APPLICATION NUMBER: 60/074086
 ; PRIOR FILING DATE: 1998-02-09
 ; PRIOR APPLICATION NUMBER: 60/074092
 ; PRIOR FILING DATE: 1998-02-09
 ; PRIOR APPLICATION NUMBER: 60/077791
 ; PRIOR FILING DATE: 1998-03-12
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/079294
 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: 60/079663
 ; PRIOR FILING DATE: 1998-02-27
 ; PRIOR APPLICATION NUMBER: 60/079728
 ; PRIOR FILING DATE: 1998-03-27
 ; PRIOR APPLICATION NUMBER: 60/080165
 ; PRIOR FILING DATE: 1998-03-31
 ; PRIOR APPLICATION NUMBER: 60/081203
 ; PRIOR FILING DATE: 1998-04-09
 ; PRIOR APPLICATION NUMBER: 60/081229
 ; PRIOR FILING DATE: 1998-04-09
 ; PRIOR APPLICATION NUMBER: 60/081695
 ; PRIOR FILING DATE: 1998-04-14
 ; PRIOR APPLICATION NUMBER: 60/081817
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/081818
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/082999
 ; PRIOR FILING DATE: 1998-04-24
 ; PRIOR APPLICATION NUMBER: 60/083322
 ; PRIOR FILING DATE: 1998-04-28
 ; PRIOR APPLICATION NUMBER: 60/083545
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/084600
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/084627
 ; PRIOR FILING DATE: 1998-05-07

; PRIOR APPLICATION NUMBER: 60/084637
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/085149
 ; PRIOR FILING DATE: 1998-05-12
 ; PRIOR APPLICATION NUMBER: 60/085323
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085338
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085339
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085579
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/086414
 ; PRIOR FILING DATE: 1998-05-22
 ; PRIOR APPLICATION NUMBER: 60/086430
 ; PRIOR FILING DATE: 1998-05-22
 ; PRIOR APPLICATION NUMBER: 60/087106
 ; PRIOR FILING DATE: 1998-05-28
 ; PRIOR APPLICATION NUMBER: 60/088026
 ; PRIOR FILING DATE: 1998-06-04
 ; PRIOR APPLICATION NUMBER: 60/088730
 ; PRIOR FILING DATE: 1998-06-10
 ; PRIOR APPLICATION NUMBER: 60/088741
 ; PRIOR FILING DATE: 1998-06-10
 ; PRIOR APPLICATION NUMBER: 60/088810
 ; PRIOR FILING DATE: 1998-06-10
 ; PRIOR APPLICATION NUMBER: 60/088858
 ; PRIOR FILING DATE: 19/98-06-11
 ; PRIOR APPLICATION NUMBER: 60/089532
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/089599
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/089907
 ; PRIOR FILING DATE: 1998-06-18
 ; PRIOR APPLICATION NUMBER: 60/089947
 ; PRIOR FILING DATE: 1998-06-19
 ; PRIOR APPLICATION NUMBER: 60/090349
 ; PRIOR FILING DATE: 1998-06-23
 ; PRIOR APPLICATION NUMBER: 60/090429
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090445
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090538
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090863
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: 60/091360
 ; PRIOR FILING DATE: 1998-07-01
 ; PRIOR APPLICATION NUMBER: 60/091519
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07

Query Match 99.6%; Score 1000; DB 4; Length 189;
 Best Local Similarity 99.5%; Pred. No. 4.4e-95;
 Matches 188; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGSRAVMLLLLPWTAQGRAVPGSSPAWTCQQLSQKLTLSAHPVGHMDLREG 60
 Db 1 MGSRAVMLLLLPWTAQGRAVPGSSPAWTCQQLSQKLTLSAHPVGHMDLREG 60
 Qy 61 DEETTNDVPHIQCGDGPQGLRDNQSFCLQRIHQGLIFYEKLKLGSDIFTGEPSSLDPSP 120
 Db 61 DEETTNDVPHIQCGDGPQGLRDNQSFCLQRIHQGLIFYEKLKLGSDIFTGEPSSLDPSP 120
 Qy 121 VAQLHASLLGLSQLLQPEGHWHWETQIPSLSPSQWQBLRLFRKILRSLOAFVAARVF 180
 Db 121 VGQLHASLLGLSQLLQPEGHWHWETQIPSLSPSQWQBLRLFRKILRSLOAFVAARVF 180

Qy 181 AHGAATLSP 189
 |||||
 Db 181 AHGAATLSP 189

RESULT 10

US-10-140-808-232
 ; Sequence 232, Application US/10140808
 ; Publication No. US20030017563A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3330R1C182
 ; CURRENT APPLICATION NUMBER: US/10/140,808
 ; CURRENT FILING DATE: 2002-05-07
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 232
 ; LENGTH: 189
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-140-808-232

Query Match 99.6%; Score 1000; DB 4; Length 189;
 Best Local Similarity 99.5%; Pred. No. 4.4e-95;
 Matches 188; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLGSRAVMLLLLPWTAQGRAVPGSSPAWTCQQLSQKLTLSAHPVLVGHMDLREEG 60
 |||||
 Db 1 MLGSRAVMLLLLPWTAQGRAVPGSSPAWTCQQLSQKLTLSAHPVLVGHMDLREEG 60
 |||||
 Qy 61 DEETTNDVPHIQCGDCDPQGLRDNSQFCQLRIHQGLIFYEKLIGSDIFTGEPSSLDPSP 120
 |||||
 Db 61 DEETTNDVPHIQCGDCDPQGLRDNSQFCQLRIHQGLIFYEKLIGSDIFTGEPSSLDPSP 120
 |||||
 Qy 121 VAQLHASLLGLSOLLQPEGHHWETQIPLSPSPQWQRLRLFKILRSLOAFVAVAAARVF 180
 |||||
 Db 121 VGQLHASLLGLSOLLQPEGHHWETQIPLSPSPQWQRLRLFKILRSLOAFVAVAAARVF 180
 |||||
 Qy 181 AHGAATLSP 189
 |||||
 Db 181 AHGAATLSP 189

RESULT 11

US-10-121-049-232
 ; Sequence 232, Application US/10121049
 ; Publication No. US20030022339A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3330R1C17
 ; CURRENT APPLICATION NUMBER: US/10/121,049
 ; CURRENT FILING DATE: 2002-04-12
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 232
 ; LENGTH: 189
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-121-049-232

Query Match 99.6%; Score 1000; DB 4; Length 189;
 Best Local Similarity 99.5%; Pred. No. 4.4e-95;
 Matches 188; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLGSRAVMLLLLPWTAQGRAVPGSSPAWTCQQLSQKLTLSAHPVLVGHMDLREEG 60
 |||||
 Db 1 MLGSRAVMLLLLPWTAQGRAVPGSSPAWTCQQLSQKLTLSAHPVLVGHMDLREEG 60
 |||||
 Qy 61 DEETTNDVPHIQCGDCDPQGLRDNSQFCQLRIHQGLIFYEKLIGSDIFTGEPSSLDPSP 120
 |||||
 Db 61 DEETTNDVPHIQCGDCDPQGLRDNSQFCQLRIHQGLIFYEKLIGSDIFTGEPSSLDPSP 120
 |||||
 Qy 121 VAQLHASLLGLSOLLQPEGHHWETQIPLSPSPQWQRLRLFKILRSLOAFVAVAAARVF 180
 |||||
 Db 121 VGQLHASLLGLSOLLQPEGHHWETQIPLSPSPQWQRLRLFKILRSLOAFVAVAAARVF 180
 |||||
 Qy 181 AHGAATLSP 189
 |||||
 Db 181 AHGAATLSP 189

RESULT 12

US-10-123-904-232
 ; Sequence 232, Application US/10123904
 ; Publication No. US20030022328A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3330R1C54
 ; CURRENT APPLICATION NUMBER: US/10/123,904
 ; CURRENT FILING DATE: 2002-04-16
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 550

```
; SEQ ID NO 232
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-904-232

Query Match          99.6%; Score 1000; DB 4; Length 189;
Best Local Similarity 99.5%; Pred. No. 4.4e-95;
Matches 188; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLGSAVMLLLPWTAGRAVPGSSPAWTCQQLSQKLTLSAHPVLGHMDLREEG 60
Db 1 MLGSAVMLLLPWTAGRAVPGSSPAWTCQQLSQKLTLSAHPVLGHMDLREEG 60

Qy 61 DEETTNDVPHIQCGDGPQGLRDNSQFCQRIHQGLIFYEKLLGSDIFTGEPSSLDPSP 120
Db 61 DEETTNDVPHIQCGDGPQGLRDNSQFCQRIHQGLIFYEKLLGSDIFTGEPSSLDPSP 120

Qy 121 VAQLHASLLGLSQQLQPEGHWHWETQOIPSLSPSQPWQRLRLRFRKILRSLOAFVAAARVF 180
Db 121 VQQLHASLLGLSQQLQPEGHWHWETQOIPSLSPSQPWQRLRLRFRKILRSLOAFVAAARVF 180

Qy 181 AHGAATLSP 189
Db 181 AHGAATLSP 189

RESULT 13
US-10-140-470-232
; Sequence 232, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC160
; CURRENT APPLICATION NUMBER: US/10/140,470
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 232
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-470-232

Query Match          99.6%; Score 1000; DB 4; Length 189;
Best Local Similarity 99.5%; Pred. No. 4.4e-95;
Matches 188; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLGSAVMLLLPWTAGRAVPGSSPAWTCQQLSQKLTLSAHPVLGHMDLREEG 60
Db 1 MLGSAVMLLLPWTAGRAVPGSSPAWTCQQLSQKLTLSAHPVLGHMDLREEG 60

Qy 61 DEETTNDVPHIQCGDGPQGLRDNSQFCQRIHQGLIFYEKLLGSDIFTGEPSSLDPSP 120
Db 61 DEETTNDVPHIQCGDGPQGLRDNSQFCQRIHQGLIFYEKLLGSDIFTGEPSSLDPSP 120

Qy 121 VAQLHASLLGLSQQLQPEGHWHWETQOIPSLSPSQPWQRLRLRFRKILRSLOAFVAAARVF 180
Db 121 VQQLHASLLGLSQQLQPEGHWHWETQOIPSLSPSQPWQRLRLRFRKILRSLOAFVAAARVF 180

Qy 181 AHGAATLSP 189
Db 181 AHGAATLSP 189

RESULT 14
US-10-175-746-232
; Sequence 232, Application US/10175746
; Publication No. US20030027270A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC353
; CURRENT APPLICATION NUMBER: US/10/175,746
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 232
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-746-232

Query Match          99.6%; Score 1000; DB 4; Length 189;
Best Local Similarity 99.5%; Pred. No. 4.4e-95;
Matches 188; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLGSAVMLLLPWTAGRAVPGSSPAWTCQQLSQKLTLSAHPVLGHMDLREEG 60
Db 1 MLGSAVMLLLPWTAGRAVPGSSPAWTCQQLSQKLTLSAHPVLGHMDLREEG 60

Qy 61 DEETTNDVPHIQCGDGPQGLRDNSQFCQRIHQGLIFYEKLLGSDIFTGEPSSLDPSP 120
Db 61 DEETTNDVPHIQCGDGPQGLRDNSQFCQRIHQGLIFYEKLLGSDIFTGEPSSLDPSP 120

Qy 121 VAQLHASLLGLSQQLQPEGHWHWETQOIPSLSPSQPWQRLRLRFRKILRSLOAFVAAARVF 180
Db 121 VQQLHASLLGLSQQLQPEGHWHWETQOIPSLSPSQPWQRLRLRFRKILRSLOAFVAAARVF 180

Qy 181 AHGAATLSP 189
Db 181 AHGAATLSP 189

RESULT 15
US-10-176-918-232
; Sequence 232, Application US/10176918
; Publication No. US20030027275A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
```

```

; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330RIC382
; CURRENT APPLICATION NUMBER: US/10/176,918
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 232
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-918-232

Query Match      99.6%; Score 1000; DB 4; Length 189;
Best Local Similarity 99.5%; Pred. No. 4.4e-95;
Matches 188; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLGSRAVMLLLLPWTAGRAVPGSSSPAWTQCQQLSQKLTLAWSAHPVGHMDLREEG 60
Db 1 MLGSRAVMLLLLPWTAGRAVPGSSSPAWTQCQQLSQKLTLAWSAHPVGHMDLREEG 60

Qy 61 DEETTNDVPHIQCGDGDPOGLRDNSQFCLQRIHQGLIFYEKLIGSDIFTGEPSSLIPDSP 120
Db 61 DEETTNDVPHIQCGDGDPOGLRDNSQFCLQRIHQGLIFYEKLIGSDIFTGEPSSLIPDSP 120

Qy 121 VAQLHASLLGLSQLQPEGHHWETQQIPSLSPSQPWQRLRLRFKILRSLOAFVAVARVF 180
Db 121 VGQLHASLLGLSQLQPEGHHWETQQIPSLSPSQPWQRLRLRFKILRSLOAFVAVARVF 180

Qy 181 AHGAATLSP 189
Db 181 AHGAATLSP 189

```

Search completed: June 20, 2006, 04:46:39
Job time : 139.436 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2006, 04:42:09 ; Search time 12.7636 Seconds
(without alignments)
334.012 Million cell updates/sec

Title: US-10-797-157-2
Perfect score: 1004
Sequence: 1 MLGSRVALLLLPWTQGR.....QAFVAVARVFAHGATLSP 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 96747 seqs, 22556637 residues

Total number of hits satisfying chosen parameters: 96747

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB_PEP.*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB_PEP.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB_PEP.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB_PEP.*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB_PEP.*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB_PEP.*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB_PEP.*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100	10.0	204	US-10-511-937-2461	Sequence 2461, Ap
2	96	9.6	174	US-11-183-218-2	Sequence 2, Appl
3	96	9.6	177	US-11-330-353-14	Sequence 14, Appl
4	96	9.6	787	US-11-330-353-16	Sequence 16, Appl
5	78.5	7.8	541	US-10-511-937-2514	Sequence 2514, Ap
6	78.5	7.8	541	US-11-293-697-4308	Sequence 4308, Ap
7	78	7.8	457	US-10-449-902-47066	Sequence 47066, A
8	78	7.8	812	US-10-449-902-42967	Sequence 42967, A
9	76.5	7.6	635	US-11-254-252-14	Sequence 14, Appl
10	76.5	7.6	1073	US-10-449-902-50549	Sequence 50549, A
11	76	7.6	330	US-10-449-902-36639	Sequence 36639, A
12	76	7.6	389	US-10-449-902-21468	Sequence 21468, A
13	76	7.6	470	US-10-953-349-21467	Sequence 21467, A
14	76	7.6	506	US-10-953-349-21466	Sequence 21466, A
15	75	7.5	290	US-10-449-902-49311	Sequence 49311, A
16	74	7.4	290	US-10-449-902-46635	Sequence 46635, A
17	73.5	7.3	319	US-10-449-902-44048	Sequence 44048, A
18	73.5	7.3	646	US-10-449-902-51369	Sequence 51369, A
19	70.5	7.0	271	US-11-293-697-3963	Sequence 3963, Ap
20	70.5	7.0	385	US-11-293-697-3636	Sequence 3636, Ap
21	70	7.0	758	US-10-449-902-52641	Sequence 52641, A
22	69.5	6.9	398	US-10-449-902-52026	Sequence 52026, A
23	69	6.9	234	US-10-505-928-507	Sequence 507, App
24	69	6.9	267	US-10-953-349-22340	Sequence 22340, A
25	69	6.9	295	US-10-953-349-22339	Sequence 22339, A

ALIGNMENTS

RESULT 1

US-10-511-937-2461
; Sequence 2461, Application US/10511937
; Publication No. US2006008836A1

GENERAL INFORMATION:

; APPLICANT: EXPRESSION DIAGNOSTICS, INC.

; APPLICANT: Wohlgemuth, Jay

; APPLICANT: Fry, Kirk

; APPLICANT: Woodward, Robert

; APPLICANT: Ly, Ngoc

; APPLICANT: Prentice, James

; APPLICANT: Morris, MacDonald

; APPLICANT: Rosenberg, Steven

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING

; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION

; FILE REFERENCE: 505612000104

; CURRENT APPLICATION NUMBER: US/10/511,937

; CURRENT FILING DATE: 2004-10-19

; PRIOR APPLICATION NUMBER: PCT/US2003/012946

; PRIOR FILING DATE: 2003-04-24

; PRIOR APPLICATION NUMBER: US 10/131,831

; PRIOR FILING DATE: 2002-04-24

; PRIOR APPLICATION NUMBER: US 10/325,899

; PRIOR FILING DATE: 2002-12-20

; NUMBER OF SEQ ID NOS: 3117

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2461

; LENGTH: 204

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-511-937-2461

Query Match 10.0%; Score 100; DB 6; Length 204;

Best Local Similarity 25.9%; Pred. No. 0.0051;

Matches 51; Conservative 20; Mismatches 76; Indels 50; Gaps 11;

QY	15	WTAGRAVPGSSPAWTO-----COQ-----LSOKLCTLAWSAHP-----LVGHM 54
DB	25	WTVQ--EATPLGPASSLPQSFLLKLCDEQVRKQGGDGAALQEKLCATYKLCPELVLLGH- 82
QY	55	DLREGBEETNDVPHIQCGDGDPCQGLRDNSSQFQRIHQGLIFYEKLLGSDIFTG-EP 113
DB	83	-----SIGIFWAPL-SSCPQALQ--LAGCLSQLHSGLFLYQGLL--QALEGISP 127
QY	114	SLLPSPVAQLHASLLGLSQLQPPGHWHWTQIIFSLSPSQ-----PWORLLLRFKI 165
DB	128	ELGPTLDTLQDVADFATTIWOQME-----ELGMAPALQPTQGMFAFASAFORAGGVLV 183

Qy 166 LRSLOAFVAVARFAH 182
 Db 184 ASHLQSFLEVSRYRLRH 200

RESULT 2

US-11-183-218-2
 ; Sequence 2, Application US/11183218
 ; Publication No. US2006008906A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Neose Technologies, Inc.
 ; APPLICANT: Defrees, Shawn
 ; APPLICANT: Zopf, David
 ; APPLICANT: Bayer, Robert
 ; APPLICANT: Hakes, David
 ; APPLICANT: Chen, Xi
 ; APPLICANT: Bowe, Carvne
 ; TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND
 ; FILE REFERENCE: 040853-01-5083-US02
 ; CURRENT APPLICATION NUMBER: US/11/183,218
 ; CURRENT FILING DATE: 2005-07-15
 ; PRIOR FILING DATE: 2003-04-09
 ; PRIOR APPLICATION NUMBER: PCT/US02/32263
 ; PRIOR FILING DATE: 2002-10-09
 ; PRIOR APPLICATION NUMBER: US 60/407,527
 ; PRIOR FILING DATE: 2002-08-28
 ; PRIOR APPLICATION NUMBER: US 60/404,249
 ; PRIOR FILING DATE: 2002-08-16
 ; PRIOR APPLICATION NUMBER: US 60/396,594
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/391,777
 ; PRIOR FILING DATE: 2002-06-25
 ; PRIOR APPLICATION NUMBER: US 60/387,292
 ; PRIOR FILING DATE: 2002-06-07
 ; PRIOR APPLICATION NUMBER: US 60/344,692
 ; PRIOR FILING DATE: 2001-11-19
 ; PRIOR APPLICATION NUMBER: US 60/334,301
 ; PRIOR FILING DATE: 2001-11-28
 ; PRIOR APPLICATION NUMBER: US 60/334,233
 ; PRIOR FILING DATE: 2001-11-28
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 75
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 2
 ; LENGTH: 174
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-11-183-218-2

Query Match 9.6%; Score 96; DB 7; Length 174;
 Best Local Similarity 26.1%; Pred. No. 0.011;
 Matches 48; Conservative 19; Mismatches 77; Indels 40; Gaps 9;
 Qy 12 LLPWTAQGRAVPGSSPAWTCQOOLSKLCTLAWSAHP-----LVGHMDLREEGDEETND 67
 Db 14 LLKCLEQVRKIQDGA-----ALQEKLCATYKLCHEPELVLLGH-----SLG 55
 Qy 68 VPHIQCGDGPGLRDNQFCLORIHOGLIFYEKLIGSDIFTG-EPSLLPDSFVAQLHA 126
 Db 56 IPWAPL-SSCPSQALQ--LAGCLSQLHSGFLYQGLL--QALEGISPELGTDLTLDQDV 110
 Qy 127 SLGLSOLLQPEGHWHWETQIPLSPSQ-----PWQRLLRFKILRSLOAFVAVAR 178
 Db 111 ADFATTIWQME-----ELGWAPALQPTQGAFAFAFORRAGGVLVASHLQSFLEVS 166
 Qy 179 VFAH 182
 Db 167 VLRH 170

RESULT 3

US-11-330-353-14
 ; Sequence 14, Application US/11330353
 ; Publication No. US20060105429A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fleer, Reinhard
 ; Fournier, Alain
 ; Guitton, Jean-Dominique
 ; Jung, Gerard
 ; Yeh, Patrice
 ; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
 ; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
 ; CONTAINING SAID POLYPEPTIDES
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Rhone-Poulenc Rorer Inc.
 ; STREET: 500 Arcola Road, 3C43
 ; CITY: Collegeville
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19426
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Macintosh
 ; OPERATING SYSTEM: System 7.1
 ; SOFTWARE: Word 5.1 (Patentin)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/11/330,353
 ; FILING DATE: 12-Jan-2006
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/237,624
 ; FILING DATE: 10-Sep-2002
 ; APPLICATION NUMBER: US/08/797,689
 ; FILING DATE: 31-JAN-1997
 ; APPLICATION NUMBER: US 08/256,927
 ; FILING DATE: 28-JUL-1994
 ; APPLICATION NUMBER: FR 92/01064
 ; FILING DATE: 31-JAN-1992
 ; APPLICATION NUMBER: PCT/FR93/00085
 ; FILING DATE: 28-JAN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith Ph.D., Julie K.
 ; REGISTRATION NUMBER: P-38,619
 ; REFERENCE/DOCKET NUMBER: ST92006-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (610) 454-3839
 ; TELEFAX: (610) 454-3808
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 177 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
 ; US-11-330-353-14

Query Match 9.6%; Score 96; DB 7; Length 177;
 Best Local Similarity 26.1%; Pred. No. 0.011;
 Matches 48; Conservative 19; Mismatches 77; Indels 40; Gaps 9;
 Qy 12 LLPWTAQGRAVPGSSPAWTCQOOLSKLCTLAWSAHP-----LVGHMDLREEGDEETND 67
 Db 17 LLKCLEQVRKIQDGA-----ALQEKLCATYKLCHEPELVLLGH-----SLG 58
 Qy 68 VPHIQCGDGPGLRDNQFCLORIHOGLIFYEKLIGSDIFTG-EPSLLPDSFVAQLHA 126
 Db 59 IPWAPL-SSCPSQALQ--LAGCLSQLHSGFLYQGLL--QALEGISPELGTDLTLDQDV 113
 Qy 127 SLGLSOLLQPEGHWHWETQIPLSPSQ-----PWQRLLRFKILRSLOAFVAVAR 178
 Db 114 ADFATTIWQME-----ELGWAPALQPTQGAFAFAFORRAGGVLVASHLQSFLEVS 169
 Qy 179 VFAH 182

Db 170 VLRH 173

RESULT 4

US-11-330-353-16

; Sequence 16, Application US/11330353

; Publication No. US20060105429A1

GENERAL INFORMATION:

APPLICANT: Fleer, Reinhard

Fournier, Alain

Guittion, Jean-Dominique

Jung, Gerard

Yeh, Patrice

TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES, PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION CONTAINING SAID POLYPEPTIDES

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSER: Rhone-Poulenc Rorer Inc.

STREET: 500 Arcola Road, 3C43

CITY: Collegeville

STATE: PA

COUNTRY: USA

ZIP: 19426

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Macintosh

OPERATING SYSTEM: System 7.1

SOFTWARE: Word 5.1 (PatentIn)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/11/330,353

FILING DATE: 12-Jan-2006

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/10/237,624

FILING DATE: 10-Sep-2002

APPLICATION NUMBER: US/08/797,689

FILING DATE: 31-Jan-1997

APPLICATION NUMBER: US 08/256,927

FILING DATE: 28-JUL-1994

APPLICATION NUMBER: FR 92/01064

FILING DATE: 31-Jan-1992

APPLICATION NUMBER: PCT/FR93/00085

FILING DATE: 28-Jan-1993

ATTORNEY/AGENT INFORMATION:

NAME: Smith Ph.D., Julie K.

REGISTRATION NUMBER: P-38,619

REFERENCE/DOCKET NUMBER: ST92006-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (610) 454-3839

TELEFAX: (610) 454-3808

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 787 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-11-330-353-16

Query Match 9.6%; Score 96; DB 7; Length 787;

Best Local Similarity 26.1%; Pred. No. 0.067; Mismatches 19; Indels 40; Gaps 9;

Matches 48; Conservative 19;

Db 12 LIPWTAQGRAVPGSSPAWTCQOOLSKLCTLAWSAHP-----LVGHMDLREGBDEETND 67

38 LKLCLEQVRKIQDGA-----ALQEKLCATYKLCHPPELVLGH-----SLG 79

68 VPHIQCGDCDQGLRDNSQFCLQRHQGLIFYEKLLGSDIFTG-EPSLLPSPVAQLHA 126

80 IPWAPL-SSCPSQALQ--LAGCLSLQHSGLFLYQGLL--QALEGISPELGLPTLDTLQLDV 134

127 SILGLSOLLQPEGHWHWTQOIPSLSPSQ-----PWORLLLRFKILRSLOAFVAAAR 178

135 ADFATTIWQME-----ELGMAPALQTOGAMPAFASAFORRAGGVIVASHLSQSFLEVSYR 190

179 VPAH 182

191 VLRH 194

RESULT 5

US-10-511-937-2514

; Sequence 2514, Application US/10511937

; Publication No. US20060088836A1

GENERAL INFORMATION:

APPLICANT: EXPRESSION DIAGNOSTICS, INC.

APPLICANT: Wohlgenuth, Jay

APPLICANT: Fry, Kirk

APPLICANT: Woodward, Robert

APPLICANT: Ly, Ngoc

APPLICANT: Prentice, James

APPLICANT: Morris, MacDonald

APPLICANT: Rosenberg, Steven

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING TRANSPLANT REJECTION

FILE REFERENCE: 506612000104

CURRENT APPLICATION NUMBER: US/10/511,937

CURRENT FILING DATE: 2004-10-19

PRIOR APPLICATION NUMBER: PCT/US2003/012946

PRIOR FILING DATE: 2003-04-24

PRIOR APPLICATION NUMBER: US 10/131,831

PRIOR FILING DATE: 2002-04-24

PRIOR APPLICATION NUMBER: US 10/325,899

PRIOR FILING DATE: 2002-12-20

NUMBER OF SEQ ID NOS: 3117

SOFTWARE: PatentIn version 3.2

SEQ ID NO 2514

LENGTH: 541

TYPE: PRT

ORGANISM: Homo sapiens

US-10-511-937-2514

Query Match 7.8%; Score 78.5; DB 6; Length 541;

Best Local Similarity 29.9%; Pred. No. 2.5;

Matches 46; Conservative 20; Mismatches 51; Indels 37; Gaps 9;

8 MLLLLPWTAGRAV-PGSSPAWTCQOOLSKLCTLAWSAHPVLVGHMDLREGBDEETN 66

389 MVHLIIP--ELGACVAPGNN-----LIVELARYL-----VDVROEQLGQFNT 428

67 DVPHIQCGDCDQ-GLRDN---SOFCLQRHQGLIFYEKLLGSDIFTGEPSSLPSPA 122

429 RVRELAQAAGFAPQIGARPSETFAFCKSQ-----ESALGNTVPAVEPGTTPDLILA 480

123 Q-LHAS---LLGLSOLLQPEGHWHWTQOIPSLSP 152

481 QPLEASNPALGLTQPLQGGTPHCEPCQLPSESP 514

RESULT 6

US-11-293-697-4308

; Sequence 4308, Application US/11293697

; Publication No. US20060105376A1

GENERAL INFORMATION:

APPLICANT: HELIX-RESEARCH INSTITUTE

TITLE OF INVENTION: Novel full length cDNA

FILE REFERENCE: H1-A0106

CURRENT APPLICATION NUMBER: US/11/293,697

CURRENT FILING DATE: 2005-12-05

PRIOR APPLICATION NUMBER: US/10/108,260

PRIOR FILING DATE: 2002-03-28

NUMBER OF SEQ ID NOS: 5458

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 4308

QY 14 PNTAQR-----AVPGSSPAW-----TQCQLSQKCLTSAHPLVGHMDL--- 56
 Db 87 FWPFLYNECGWAGWLLSPRGPRGWPDPDRRRGRNLGKVIDTITTCGFADLWGIPLVY 146
 QY 57 ---REGBETTNDVPH-----TQCGD-----GCDPQGLRDNQFCLQRIHQGLIFYEKL 103
 Db 147 QVNSSGLVHTVNDPCNSSIVYEADAIIHTFGVPCVREGNASCWVAVTPVATRDGK 206
 QY 104 LGS-----DFTCEPSLLPSPVAQLHASLGLSQL--LOPEGHWHETQIIP-SLSPS 153
 Db 207 LPTQLRRHIDLLVGSATLCSALYVGDLCGSVFLVQLFTFSFR-RHWTTCDCNCSIYPG 265
 QY 154 -----QWQRL-----LLREFKILRSLOAFVAAARV 179
 Db 266 HITGRMAWMMNWSPTAALVVAQLLRIPQAIMDMETHV 305

RESULT 10
 US-10-449-902-50549
 ; Sequence 50549, Application US/10449902
 ; Publication No. US20060123505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: National Institute of Agrobiological Sciences.
 ; APPLICANT: Bio-oriented Technology Research Advancement Institution.
 ; APPLICANT: The Institute of Physical and Chemical Research.
 ; APPLICANT: Foundation for Advancement of International Science.
 ; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
 ; FILE REFERENCE: MOA-A0205Y1-US
 ; CURRENT APPLICATION NUMBER: US/10/449,902
 ; CURRENT FILING DATE: 2003-05-29
 ; PRIOR APPLICATION NUMBER: JP 2002-203269
 ; PRIOR FILING DATE: 2002-05-30
 ; PRIOR APPLICATION NUMBER: JP 2002-383870
 ; PRIOR FILING DATE: 2002-12-11
 ; NUMBER OF SEQ ID NOS: 56791
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 50549
 ; LENGTH: 1073
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 US-10-449-902-50549

Query Match 7.6%; Score 76.5; DB 6; Length 1073;
 Best Local Similarity 26.2%; Pred. No. 9.3;
 Matches 27; Conservative 12; Mismatches 41; Indels 23; Gaps 4;
 QY 44 AWSAHPVLGHMDLR---BEGDETTNDVPHI-QCGDGDPCQGLRDNQFCLQRIHQGLIF 99
 Db 147 AWRWARLGHINFRALCKWKEELVYRGLPCLSQVDQVCEA-----CLARKHRRSPF 197
 QY 100 YKLLGSDIFTGERSLLPSPVAQLHASLGLSQLLOPEGHWH 142
 Db 198 PRQAL-----CRSDEPLALLHGLCGPITPATPSGNRY 230

RESULT 11
 US-10-449-902-36639
 ; Sequence 36639, Application US/10449902
 ; Publication No. US20060123505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: National Institute of Agrobiological Sciences.
 ; APPLICANT: Bio-oriented Technology Research Advancement Institution.
 ; APPLICANT: The Institute of Physical and Chemical Research.
 ; APPLICANT: Foundation for Advancement of International Science.
 ; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
 ; FILE REFERENCE: MOA-A0205Y1-US
 ; CURRENT APPLICATION NUMBER: US/10/449,902
 ; CURRENT FILING DATE: 2003-05-29
 ; PRIOR APPLICATION NUMBER: JP 2002-203269
 ; PRIOR FILING DATE: 2002-05-30
 ; PRIOR APPLICATION NUMBER: JP 2002-383870
 ; PRIOR FILING DATE: 2002-12-11

; NUMBER OF SEQ ID NOS: 56791
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 36639
 ; LENGTH: 330
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 US-10-449-902-36639

Query Match 7.6%; Score 76; DB 6; Length 330;
 Best Local Similarity 21.8%; Pred. No. 2.5;
 Matches 42; Conservative 21; Mismatches 68; Indels 62; Gaps 8;

QY 5 RAVMLLLPMTAQGRAVPGSSPAWQ-----CQQLSQK-----LCTLAWSAH 48
 Db 60 RVYLEILTIPLIGVYIQQSLVYTTNGLITVAQQLSLKNDVAKVKVGLPTRAHQKF 119
 QY 49 PLVGHMDLRE-----EGDETTNDVPHIQCGDGDPCQGLRDNQFCLQRIHQ 95
 Db 120 PRVGHKMMQERPLEDAHMHMTLSTNNETANNIMEGKVSASSSPEELLEQA---LQHLET 176
 QY 96 GLIFYEKLKLSGDIPTGEPSSLP-----DSPVAQLHASLGLSQL-----LOPEGHWH 142
 Db 177 G-----NQDAIPLIRTAIEKDS---SLYVALIGMGQTILFSNRLFPEATVC 219
 QY 143 ETQQIPSLSPSQP 155
 Db 220 FEHAIPKIEEQDP 232

RESULT 12
 US-10-953-349-21468
 ; Sequence 21468, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nikolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; CURRENT FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 21468
 ; LENGTH: 389
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 US-10-953-349-21468

Query Match 7.6%; Score 76; DB 6; Length 389;
 Best Local Similarity 26.2%; Pred. No. 3;
 Matches 32; Conservative 21; Mismatches 35; Indels 34; Gaps 7;
 QY 82 LRDNQFCLQRIHQGLIFYEKLKLSGDIPTGEPSSLPSPVAQLH-ASLLG----- 130
 Db 85 LEDGTGIKAVKMEHGVISSKAL---EEFQABIAVL--SKVRHRLVSLGLYSIDGNERLL 139
 QY 131 -----LSQLLOPEGHWHETQIIPSLSPSQPW-QRLLLRFKILRSLOAFVAAARV 180
 Db 140 VYEYMSLGLALSQHL-----FHWKSLKLEPLS-----WSQRLATALDVARGMEYHLHSLARQTF 191
 QY 181 AH 182
 Db 192 IH 193

RESULT 13
 US-10-953-349-21467
 ; Sequence 21467, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nikolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; FILE REFERENCE: ENCODED THERBY

```

; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21467
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-21467

Query Match      7.6%; Score 76; DB 6; Length 470;
Best Local Similarity 26.2%; Pred. No. 3.8;
Matches 32; Conservative 21; Mismatches 35; Indels 34; Gaps 7;

Qy 82 LRDNQFCLRIHQGLIFYEKLLGSDIFTGSPSLPSPAQLH-ASLLG----- 130
Db 166 LEDGTKIAXKMEHGVISSKAL---EFQAEIAYL--SKVHRHLVSLGYSIDGNERLL 220
Qy 131 -----LSQLQPEGHWHETOQIPSLSPSPW-QRLLLRFKILRSLOAFVAAARVF 180
Db 221 VVEYMSLGALSQHL-----FWKSKLRLPLS-----WSQRLAIALDVARGMEYLSLARQTF 272
Qy 181 AH 182
Db 273 IH 274

RESULT 14
US-10-953-349-21466
; Sequence 21466, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21466
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-21466

Query Match      7.6%; Score 76; DB 6; Length 506;
Best Local Similarity 26.2%; Pred. No. 4.2;
Matches 32; Conservative 21; Mismatches 35; Indels 34; Gaps 7;

Qy 82 LRDNQFCLRIHQGLIFYEKLLGSDIFTGSPSLPSPAQLH-ASLLG----- 130
Db 202 LEDGTKIAXKMEHGVISSKAL---EFQAEIAYL--SKVHRHLVSLGYSIDGNERLL 256
Qy 131 -----LSQLQPEGHWHETOQIPSLSPSPW-QRLLLRFKILRSLOAFVAAARVF 180
Db 257 VVEYMSLGALSQHL-----FWKSKLRLPLS-----WSQRLAIALDVARGMEYLSLARQTF 308
Qy 181 AH 182
Db 309 IH 310

RESULT 15
US-10-449-902-49311
; Sequence 49311, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.

```

```

; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449.902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49311
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-49311

Query Match      7.5%; Score 75; DB 6; Length 290;
Best Local Similarity 22.9%; Pred. No. 2.7;
Matches 44; Conservative 35; Mismatches 69; Indels 44; Gaps 11;

Qy 12 LLPWTAQGRAV-PGGSSPAWTQCQQLSQKLCITLAWSAHPL-----VGHMDLREEGDEE 63
Db 98 LISWSQGENEVFEGSWDWT-----SRRVLEKSGKDHITLLVLPSPGVYHRIIVDGEPK 152
Qy 64 TTNDVPHI-----QCGDGC-----PQGLRDNQFCLRIHQGLIFYE-KLGSDFITGE 112
Db 153 YVPELPHVADEGGQVANLLDVHYIPESLGSVAGFDSPPSHEH--SYDLQLPGDEEFAKE 210
Qy 113 PSLLPDSPPVAQLHASLLG-----LSQLQPEG---HH-----WETQOIPSLSPSPQWR 158
Db 211 PPILP-----POLVMSVLGDTDNSEETLKPKNHVVLNHLHYIEKMGWSQSLALGVTHTRFQS 266
Qy 159 LLRLRFKILRSIQ 170
Db 267 KYVSFVLYKPLR 278

Search completed: June 20, 2006, 04:47:11
Job time : 13.7636 secs

```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2006, 04:47:05 ; Search time 143.345 Seconds
(without alignments)
602.837 Million cell updates/sec

Title: US-10-797-157-2

Perfect score: 189

Sequence: 1 MLGSRVALLLLPWTAGR.....QAFVAAVAFHGAATLSP 189

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2589679 seqs, 457216429 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2589342

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A Geneseq 8:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*
- 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	189	100.0	189	2 AAW95002	Human int
2	189	100.0	189	2 AAY29783	Human int
3	189	100.0	189	3 AAB01981	Human int
4	189	100.0	189	4 AAB47120	Human IL-
5	189	100.0	189	6 ABU08268	Human int
6	189	100.0	189	6 ABG75811	Human int
7	189	100.0	189	7 ADF70612	Human int
8	189	100.0	189	8 ADQ14469	Human int
9	189	100.0	189	8 ADS73601	Human IL-
10	189	100.0	189	9 ADV98151	Human p19
11	189	100.0	189	9 AEA51094	Human int
12	189	100.0	189	9 AEB47331	Human int
13	170	89.9	521	8 ADQ14473	Human hyp
14	170	89.9	521	8 ADS73607	Human IL-
15	121	64.0	189	3 AAY94966	Human sec
16	121	64.0	189	3 AAY54606	SGRF prot
17	121	64.0	189	4 AAU12287	Human PRO
18	121	64.0	189	4 AAB48070	Human ext
19	121	64.0	189	6 ABO17731	Novel hum
20	121	64.0	189	6 ABU80985	Human PRO
21	121	64.0	189	6 ABU66685	Human PRO
22	121	64.0	189	6 ABU59766	Novel sec
23	121	64.0	189	6 ABO24956	Human sec

24	121	64.0	189	6 ABU66961	Human sec
25	121	64.0	189	6 ADA45751	Novel hum
26	121	64.0	189	6 ADA76182	Human PRO
27	121	64.0	189	6 ADA18832	Human PRO
28	121	64.0	189	6 ADA61455	Homo sapi
29	121	64.0	189	6 ADB19240	Novel hum
30	121	64.0	189	6 ADB27781	Human PRO
31	121	64.0	189	6 ADA86260	Novel hum
32	121	64.0	189	6 ADB15824	Human PRO
33	121	64.0	189	6 ADA47610	Human PRO
34	121	64.0	189	6 ADA67405	Human PRO
35	121	64.0	189	6 ADB30412	Human PRO
36	121	64.0	189	6 ADA85708	Novel hum
37	121	64.0	189	6 ADA96920	Human PRO
38	121	64.0	189	6 ADA79224	Human PRO
39	121	64.0	189	6 ADA87363	Novel hum
40	121	64.0	189	6 ADB16565	Human PRO
41	121	64.0	189	6 ADA91657	Novel hum
42	121	64.0	189	6 ADB14720	Human PRO
43	121	64.0	189	6 ADB18681	Novel hum
44	121	64.0	189	6 ADA93896	Human PRO
45	121	64.0	189	6 ADB19792	Novel hum

ALIGNMENTS

RESULT 1

AAW95002
ID AAW95002 standard; protein; 189 AA.

AC AAW95002;

DT 21-MAY-1999 (first entry)

DE Human interleukin-B30 (IL-B30) polypeptide.

KW Cytokine; interleukin-B30; IL-B30; forensic science; cell proliferation;
KW inflammatory condition; drug screening; human.

OS Homo sapiens.

Key Location/Qualifiers

Peptide 1..21

Protein /note= "signal peptide"

FT 22..189

FT /note= "mature protein"

PN WO9905280-A1.

PD 04-FEB-1999.

PF 24-JUL-1998; 98WO-US015423.

PR 25-JUL-1997; 97US-00900905.

PA (SCHE) SCHERING CORP.

PI Bazan JF;

DR WPI; 1999-142935/12.

XX N-PSDB; AAX17786.

PT Newly isolated or recombinant polynucleotide encoding mammalian cytokine
interleukin-B30 (IL-B30), including fragments - useful for regulating
activation, development, differentiation and function of various cell
types, and for diagnosing and treating conditions associated with IL-B30.

PS Claim 2; Page 8-9; 83pp; English.

CC This represents a human cytokine interleukin-B30 (IL-B30) polypeptide.
Host cells containing a vector comprising the IL-B30 nucleic acid are
used for the recombinant production of the protein. The polynucleotides

CC are useful for diagnosis of IL-B30 mediated conditions, and forensic
 CC science (e.g. to distinguish rodent from human, or as a marker to
 CC distinguish between different cells exhibiting differential expression or
 CC modification patterns). The IL-B30 (including fragments), together with
 CC antibodies that bind to IL-B30 are useful for teaching purposes. They are
 CC also used for treating conditions associated with abnormal physiology or
 CC development, including inflammatory conditions. The polypeptide cytokine
 CC should mediate cytokine synthesis and proliferation in cells. IL-B30 is
 CC useful for drug screening to identify compounds having binding affinity
 CC to IL-B30
 XX
 SQ Sequence 189 AA;

Query Match 100.0%; Score 189; DB 2; Length 189;
 Best Local Similarity 100.0%; Pred. No. 1.4e-172;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGSRVAMLLLLPWTAGRAVPGSSPAWTCQQLSOKLCTLAWSAHPVLGHMDLREEG 60
 DB 1 MLGSRVAMLLLLPWTAGRAVPGSSPAWTCQQLSOKLCTLAWSAHPVLGHMDLREEG 60
 QY 61 DEETNDVPHIQCGDGDGCDPQGLRDNSQFCQLRIHQGLIFVEKLLGSDIFTGEPSSLDPSP 120
 DB 61 DEETNDVPHIQCGDGDGCDPQGLRDNSQFCQLRIHQGLIFVEKLLGSDIFTGEPSSLDPSP 120
 QY 121 VAQLHASLLGLSOLLQPEGHMETQIIPSLSPSPQWQRLRLFKILRSLOAFVAAARVF 180
 DB 121 VAQLHASLLGLSOLLQPEGHMETQIIPSLSPSPQWQRLRLFKILRSLOAFVAAARVF 180
 QY 181 AHGAATLSP 189
 DB 181 AHGAATLSP 189

RESULT 2
 AAY29783
 ID AAY29783 standard; protein; 189 AA.
 XX
 AC AAY29783;
 XX
 DT 04-NOV-1999 (first entry)
 XX
 DE Human interleukin B30.
 XX
 KW DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;
 KW interleukin B30; DCRS1; DCRS1; IL-B30; cytokine receptor; diagnosis;
 KW inflammatory disorder; inflammatory response; innate immunity;
 KW morphogenic development; immunological disorder.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..21
 FT /label= signal
 FT Protein 22..189
 FT /label= IL-B30
 XX
 XX WO9940195-A1.
 XX
 XX 12-AUG-1999.
 XX
 XX 05-FEB-1999; 99WO-US002600.
 XX
 XX 06-FEB-1998; 98US-0073941P.
 XX 13-MAY-1998; 98US-00078194.
 XX
 XX (SCHE) SCHERING CORP.
 XX
 XX Mattson JD, Mcclanahan TK, Kastelein RA;
 XX WPI; 1999-527306/44.
 XX N-PSDB; AA208865.
 XX

PT New receptor subunits useful in the treatment inflammatory disorders.
 XX Claim 2; Page 26-27; 133pp; English.
 PS
 XX
 CC The present invention describes a composition (I) comprising DNAX
 CC cytokine receptor subunit 1 (DCRS1) protein and DNAX soluble receptor
 CC subunit 1 (DCRS1) protein, which together encode a new mammalian cytokine
 CC -related receptor (R), or DCRS1 and interleukin B30 (IL-B30) proteins, or
 CC DCRS1 and IL-B30 proteins. (I) comprising DCRS1 and DCRS1 is useful for
 CC screening for ligands (i.e. agonists/antagonists) from a library of
 CC compounds, which are useful for modulating the physiology or development
 CC of a cell or tissue culture e.g. inflammatory responses, innate immunity
 CC and/or morphogenic development. (R), antibodies and ligands are useful
 CC for treatment of conditions, especially immunological disorders,
 CC associated with conditions exhibiting abnormal expression of (R). (R) is
 CC useful as a phosphate labeling enzyme to label substrates, and the
 CC subunits DCRS1 and DCRS1 are useful as immunogens for generating
 CC antibodies, or as antigens for binding antibodies. Nucleic acids encoding
 CC (R) are useful for identifying related DNAs and mRNAs, and variants from
 CC other individuals or species. The present sequence represents the
 CC specifically claimed human IL-B30, for use in the composition of the
 CC present invention
 XX
 SQ Sequence 189 AA;

Query Match 100.0%; Score 189; DB 2; Length 189;
 Best Local Similarity 100.0%; Pred. No. 1.4e-172;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGSRVAMLLLLPWTAGRAVPGSSPAWTCQQLSOKLCTLAWSAHPVLGHMDLREEG 60
 DB 1 MLGSRVAMLLLLPWTAGRAVPGSSPAWTCQQLSOKLCTLAWSAHPVLGHMDLREEG 60
 QY 61 DEETNDVPHIQCGDGDGCDPQGLRDNSQFCQLRIHQGLIFVEKLLGSDIFTGEPSSLDPSP 120
 DB 61 DEETNDVPHIQCGDGDGCDPQGLRDNSQFCQLRIHQGLIFVEKLLGSDIFTGEPSSLDPSP 120
 QY 121 VAQLHASLLGLSOLLQPEGHMETQIIPSLSPSPQWQRLRLFKILRSLOAFVAAARVF 180
 DB 121 VAQLHASLLGLSOLLQPEGHMETQIIPSLSPSPQWQRLRLFKILRSLOAFVAAARVF 180
 QY 181 AHGAATLSP 189
 DB 181 AHGAATLSP 189

RESULT 3
 AAB01981
 ID AAB01981 standard; protein; 189 AA.
 XX
 AC AAB01981;
 XX
 DT 27-SEP-2000 (first entry)
 XX
 DE Human interleukin-B30 (IL-B30).
 XX
 KW Interleukin-B30; IL-B30; human; cytokine; cellular signalling;
 KW immune response; haematopoietic cell; IL-6 homologue; GCSF homologue;
 KW granulocyte colony stimulating factor; immune disorder;
 KW inflammatory disease; autoimmune disease; antigen; antibody.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..21
 FT /note= "Signal peptide"
 FT Protein 22..189
 FT /note= "Mature human IL-B30"
 XX
 XX US060284-A.
 XX 09-MAY-2000.
 XX

PF 24-JUL-1998; 98US-00122443.
 XX
 PR 25-JUL-1997; 97US-0053765P.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 PI Bazan JF;
 XX
 DR WPI: 2000-364420/31.
 DR N-PSDB; AAA52577.
 XX
 PT Novel recombinant DNA encoding cytokines especially interleukin-B30
 PT useful as probes or primers for diagnosing immune disorders including
 PT autoimmune or chronic inflammatory conditions.
 XX
 PS Claim 1; Col 5-8; 32pp; English.
 XX
 CC This sequence represents human interleukin-B30 (IL-B30). IL-B30 is a
 CC novel cytokine, exhibiting significant homology to IL-6 and GCSF
 CC (granulocyte colony stimulating factor). Cytokines play a critical role
 CC in signalling between immune or other cells during an immune response.
 CC The precise role of IL-B30 is not yet known - it is likely to have either
 CC a stimulatory or an inhibitory effect on haematopoietic cells such as T-
 CC cells, B-cells, natural killer (NK) cells and macrophages. Alternatively,
 CC it may affect vascular physiology or development, or have neuronal
 CC effects. IL-B30, its fragments, IL-B30 nucleotides, agonists and
 CC antagonists are useful in the diagnosis and treatment of disorders
 CC associated with abnormal expression or activity of IL-B30 e.g.,
 CC inflammatory or autoimmune disorders. Nucleotides encoding IL-B30 are
 CC useful for recombinant expression of IL-B30 in a host cell, and as a
 CC source of probes and primers. The IL-B30 probes and primers can be used
 CC to detect levels of IL-B30 expression in samples from patients suspected
 CC of having an inflammatory or autoimmune disorder. IL-B30 nucleotides may
 CC also be used to identify homologous genes in other species. IL-B30
 CC protein or its fragments are useful as antigens for raising antibodies to
 CC various linear and conformational epitopes. Such antibodies may be used
 CC to detect levels of IL-B30 protein in a sample
 XX
 SQ Sequence 189 AA;
 Query Match 100.0%; Score 189; DB 3; Length 189;
 Best Local Similarity 100.0%; Pred. No. 1.4e-172;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGSRVAVMLLLPWTAGRAVPGSSPAWTCQQLSQKLCITLAWSAHPLVGHMDLREG 60
 DB 1 MLGSRVAVMLLLPWTAGRAVPGSSPAWTCQQLSQKLCITLAWSAHPLVGHMDLREG 60
 QY 61 DEETTNDVPHIQCGDCDQGLRDNQSQCFLQRIHQGLIFYEKLGSDFITGSPSLPDSP 120
 DB 61 DEETTNDVPHIQCGDCDQGLRDNQSQCFLQRIHQGLIFYEKLGSDFITGSPSLPDSP 120
 QY 121 VAQLHASLGLSLLQLQPEGHWHETQIIPSLSPSQPWQRLLRFLKILRSIQAFVAVARVF 180
 DB 121 VAQLHASLGLSLLQLQPEGHWHETQIIPSLSPSQPWQRLLRFLKILRSIQAFVAVARVF 180
 QY 181 AHGAATLSP 189
 DB 181 AHGAATLSP 189
 RESULT 4
 AAB47120
 ID AAB47120 standard; protein; 189 AA.
 XX
 AC AAB47120;
 XX
 DT 04-JUN-2001 (first entry)
 XX
 DE Human IL-B30.
 XX
 KW Human; mouse; interleukin-B30; IL-12 p40; IL-B30; interferon-gamma;
 KW IFNgamma; Th1 response; autoimmune disease; chronic inflammation;
 KW memory T-cell; leukocyte; rheumatoid arthritis; osteoarthritis;
 KW atherosclerosis; multiple sclerosis; vasculitis; spinal injury;
 KW delayed hypersensitivity; skin graft; transplant; cancer; stroke;
 KW neurodegeneration; ischaemia; postmenopausal osteoporosis;
 KW Castleman's disease.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..21
 FT /note= "Signal peptide"
 FT Protein 22..189
 FT /note= "Mature protein"
 XX
 FN WO200118051-A2.
 XX
 PD 15-MAR-2001.
 XX
 PF 08-SEP-2000; 2000WO-US024686.
 XX
 PR 09-SEP-1999; 99US-00393090.
 PR 10-NOV-1999; 99US-0164616P.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 PI Opmann B, De Waal Malefyt R, Rennick DM, Kastelein RA;
 PI Wiekowski MT, Lira SA, Narula SK;
 XX
 DR WPI: 2001-244560/25.
 DR N-PSDB; AAC85540.
 XX
 CC Composition comprising interleukin-12 p40 and IL-B30 polypeptide or its
 CC segment, useful for ameliorating rheumatoid arthritis, osteoarthritis,
 CC atherosclerosis, multiple sclerosis, vasculitis and tumor.
 XX
 PS Disclosure; Page 10-11; 69pp; English.
 XX
 CC This sequence shows human interleukin-B30. Fragments of this protein may
 CC be used in the composition of the invention. The composition comprises a
 CC substantially pure polypeptide comprising a number of distinct segments
 CC of at least 7 contiguous amino acids from IL-12 p40 and/or IL-B30, and a
 CC substantially pure polypeptide comprising a segment of at least 11
 CC contiguous amino acids from IL-12 p40 and/or IL-B30. The composition is
 CC useful for modulating physiology or development of a cell or tissue in a
 CC host organism, resulting in an increased or decreased production of
 CC interferon-gamma (IFNgamma), an enhanced Th1 response such as anti-tumour
 CC effect, adjuvant effect, anti-viral effect or antagonized allergic
 CC effect, and amelioration of an autoimmune condition or a chronic
 CC inflammatory condition. IL-B30 or its agonist is useful inducing the
 CC proliferation of memory T-cells. An agonist or antagonist of IL-B30
 CC protein is useful for modulating the trafficking or activation of a
 CC leukocyte in an animal experiencing science or symptoms of autoimmunity,
 CC an inflammatory condition, tissue specific autoimmunity, degenerative
 CC autoimmunity, rheumatoid arthritis, osteoarthritis, atherosclerosis,
 CC multiple sclerosis, vasculitis, delayed hypersensitivities, skin
 CC grafting, a transplant, spinal injury, stroke, neurodegeneration, an
 CC infectious disease, ischaemia, cancer, tumour, multiple myeloma,
 CC Castleman's disease, postmenopausal osteoporosis or IL-6-associated
 CC diseases. IL-12 p40/IL-B30 is useful as an immunogen for the production a
 CC antisera or antibodies specific for binding
 XX
 SQ Sequence 189 AA;
 Query Match 100.0%; Score 189; DB 4; Length 189;
 Best Local Similarity 100.0%; Pred. No. 1.4e-172;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGSRVAVMLLLPWTAGRAVPGSSPAWTCQQLSQKLCITLAWSAHPLVGHMDLREG 60
 DB 1 MLGSRVAVMLLLPWTAGRAVPGSSPAWTCQQLSQKLCITLAWSAHPLVGHMDLREG 60
 QY 61 DEETTNDVPHIQCGDCDQGLRDNQSQCFLQRIHQGLIFYEKLGSDFITGSPSLPDSP 120
 DB 61 DEETTNDVPHIQCGDCDQGLRDNQSQCFLQRIHQGLIFYEKLGSDFITGSPSLPDSP 120
 QY 121 VAQLHASLGLSLLQLQPEGHWHETQIIPSLSPSQPWQRLLRFLKILRSIQAFVAVARVF 180
 DB 121 VAQLHASLGLSLLQLQPEGHWHETQIIPSLSPSQPWQRLLRFLKILRSIQAFVAVARVF 180
 QY 181 AHGAATLSP 189
 DB 181 AHGAATLSP 189

Db 61 DEETNDVPHIQCGDGPQGLRDNSQFCQRIHQGLIFYEKLGLSDIFTGEPSSLDPSP 120
 Qy 121 VAQLHASLLGLSQQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFKILRSLOAFVAAARVF 180
 Db 121 VAQLHASLLGLSQQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFKILRSLOAFVAAARVF 180
 Qy 181 AHGAATLSP 189
 Db 181 AHGAATLSP 189
 RESULT 5
 ABU08268
 ID ABU08268 standard; protein; 189 AA.
 AC ABU08268;
 XX
 DT 19-MAY-2003 (first entry)
 DE Human interleukin-B30, IL-B30.
 KW Human; interleukin-B30; IL-B30; inflammation; lymphoid cell;
 KW immunosuppressive; autoimmune disorder; immunomodulatory;
 KW anti-inflammatory; vascular; neuroprotective; immunological response;
 KW haematopoietic cell disorder; vascular physiology; development.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..21
 FT /label= Signal_peptide
 FT Protein 22..189
 FT /label= Mature IL B30
 FT /note= "This protein is specifically claimed in claim 3"
 XX
 PN USG495667-B1.
 XX
 PD 17-DEC-2002.
 XX
 XX 25-APR-2000; 2000US-00558087.
 XX
 XX 25-JUL-1997; 97US-0053765P.
 PR 24-JUL-1998; 98US-00122443.
 XX
 XX (SCHE) SCHERING CORP.
 PA
 XX Bazan JF;
 XX
 XX WPI; 2003-327470/31.
 DR N-PSDB; ABX13358.
 XX
 XX Binding compounds comprising antibodies which bind to Interleukin B30,
 PR useful for treating disorders associated with hematopoietic cells, e.g.
 PT inflammation and autoimmune diseases and development disorders.
 XX
 XX Claim 1; Col 5-6; 31pp; English.
 PS
 XX The invention relates to a binding compound comprising an antibody
 CC binding site which specifically binds to residues 1-168 (mature human
 CC interleukin-B30, IL-B30). Also included is a method of making the binding
 CC composition, comprising administering to an animal: (a) a substantially
 CC pure and isolated polypeptide comprising residues 1-168 of mature human
 CC IL-B30; (b) a substantially pure and isolated polypeptide comprising
 CC residues 1-175 of a mouse IL-B30; and/or (c) a substantially pure or
 CC isolated polypeptide comprising pig mature IL-B30. The animal produces
 CC the binding compound. The binding compound may be administered to treat
 CC disorders associated with haematopoietic cells, e.g., lymphoid cells,
 CC which affect immunological responses, e.g., inflammation and/or
 CC autoimmune disorders. Alternatively, it may affect vascular physiology or
 CC development, or neuronal effects. The present sequence represents full-
 CC length human IL-B30
 XX
 XX Sequence 189 AA;

Query Match 100.0%; Score 189; DB 6; Length 189;
 Best Local Similarity 100.0%; Pred. No. 1.4e-172;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MLGSRVALLLLPWTAAQRAVFGGSSPAWTCQQLSQKLTCLAWSAHPLVGHMDLREEG 60
 Db 1 MLGSRVALLLLPWTAAQRAVFGGSSPAWTCQQLSQKLTCLAWSAHPLVGHMDLREEG 60
 Qy 61 DEETNDVPHIQCGDGPQGLRDNSQFCQRIHQGLIFYEKLGLSDIFTGEPSSLDPSP 120
 Db 61 DEETNDVPHIQCGDGPQGLRDNSQFCQRIHQGLIFYEKLGLSDIFTGEPSSLDPSP 120
 Qy 121 VAQLHASLLGLSQQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFKILRSLOAFVAAARVF 180
 Db 121 VAQLHASLLGLSQQLOPEGHWHWTQIIPSLSPSPQWQRLRLRFKILRSLOAFVAAARVF 180
 Qy 181 AHGAATLSP 189
 Db 181 AHGAATLSP 189
 RESULT 6
 ABG75811
 ID ABG75811 standard; protein; 189 AA.
 XX
 AC ABG75811;
 XX
 DT 09-MAY-2003 (first entry)
 DE Human interleukin-B30 (IL-B30).
 XX
 KW Human; antigenic; cytokine; interleukin-B30; IL-B30; protein therapy;
 KW inflammatory condition; autoimmune disorder; activation; development;
 KW differentiation; function; haematopoietic cell; lymphoid cell; immunogen;
 KW antiinflammatory; immunosuppressive.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..21
 FT /label= Signal_peptide
 FT Protein 22..189
 FT /label= Mature_IL-B30_protein
 XX
 PN US6479634-B1.
 XX
 PD 12-NOV-2002.
 XX
 XX 25-APR-2000; 2000US-00558089.
 PF
 XX 25-JUL-1997; 97US-0053765P.
 PR 24-JUL-1998; 98US-00122443.
 XX
 XX (SCHE) SCHERING CORP.
 PA
 XX Bazan JF;
 XX
 XX WPI; 2003-298116/29.
 DR N-PSDB; ABX11988.
 XX
 XX New interleukin-B30 (IL-B30) polypeptide, useful for diagnosing or
 FT treating e.g. inflammatory conditions or autoimmune disorders, or in
 FT regulating the development of hematopoietic cells or lymphoid cells.
 PT
 XX
 XX Claim 2; Col 5-8; 31pp; English.
 PS
 XX The invention discloses an isolated antigenic mature polypeptide that is
 CC a mammalian cytokine designated interleukin-B30 (IL-B30). The IL-B30
 CC polypeptide is useful for diagnosing or treating (e.g. protein therapy)
 CC conditions associated with abnormal physiology or development (e.g.
 CC inflammatory conditions or autoimmune disorders), or in regulating the
 CC activation, development, differentiation and function of haematopoietic

CC cells or lymphoid cells. The IL-B30 polypeptide is also useful as an
 CC immunogen for producing antisera or antibodies specific for binding. The
 CC sequence presented is the human IL-B30 protein

XX Sequence 189 AA;

Query Match 100.0%; Score 189; DB 6; Length 189;
 Best Local Similarity 100.0%; Pred. No. 1.4e-172;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGSAVMLLLPMTAQGRAVPGSSPAWTCQQLSQKLTAWSAHPLVGHMDLREG 60
 DB 1 MLGSAVMLLLPMTAQGRAVPGSSPAWTCQQLSQKLTAWSAHPLVGHMDLREG 60
 QY 61 DEETNDVPHICGDCDQGLRDNSQFCQRIHQGLIFYEKLGSDIFTGSPSLPDS 120
 DB 61 DEETNDVPHICGDCDQGLRDNSQFCQRIHQGLIFYEKLGSDIFTGSPSLPDS 120
 QY 121 VAQLHASLGLSOLLQPEGHWHWTQIPLSPSPQWQRLRLFKILRSLOAFVAVARVF 180
 DB 121 VAQLHASLGLSOLLQPEGHWHWTQIPLSPSPQWQRLRLFKILRSLOAFVAVARVF 180
 QY 181 AHGAATLSP 189
 DB 181 AHGAATLSP 189

RESULT 7

ID ADF70612 standard; protein; 189 AA.

XX ADF70612;

DT 12-FEB-2004 (first entry)

XX Human interleukin B30.

KW Human; interleukin B30; IL-B30; IL-12 p40; tumour necrosis factor alpha;
 KW IFN-alpha; interferon alpha; chronic inflammatory condition;
 KW memory T-cell; tumour; anti-viral; vaccine; allergic responses;
 KW autoimmune disease; multiple sclerosis; rheumatoid arthritis;
 KW inflammatory bowel disease; psoriasis.

XX Homo sapiens.

XX US2003162261-A1.

XX 28-AUG-2003.

XX 27-FEB-2003; 2003US-00375706.

XX 09-SEP-1999; 99US-0153281P.

XX 10-NOV-1999; 99US-0164616P.

XX 08-SEP-2000; 2000US-00638699.

XX (SCHE) SCHERING CORP.

XX Oppmann B, De Waal Malefyt R, Rennick DM, Kastelein RA;

XX Wiekowski MT, Lira SA, Narula SK;

XX WPI; 2003-897932/82.

XX N-PSDB; ADF70611.

XX Composition comprising fragments from interleukin (IL)-12 p40 and IL-B30

XX polypeptides is useful to enhance anti-viral, anti-tumor and vaccine
 XX effects and to antagonize allergic responses.
 XX Example 2; SEQ ID NO 2; 34pp; English.
 XX The invention relates to a composition comprising polypeptide fragments
 CC from interleukin (IL)-12 p40 and IL-B30 is new. The fragments comprise 7
 CC or 11 contiguous amino acids. Also included are an isolated or
 CC recombinant nucleic acid (NI) encoding the polypeptides of the novel

CC composition, a cell comprising recombinant NI, a nucleic acid which
 CC hybridises the natural coding portion of primate IL-12 p40 and primate IL
 CC -30, an antagonist of IL-12 p40/IL-B30 (combined with a tumour necrosis
 CC factor (TNF) alpha antagonist, an IL-12 antagonist, IL-10 or steroids), a
 CC binding compound comprising an antigen binding site from an antibody
 CC which specifically binds to the novel composition, producing an
 CC antigen-antibody complex, modulating physiology or development of a cell
 CC or tissue (comprising contacting the cell with the claimed composition to
 CC increase production of IFN-alpha, modulating physiology or development of
 CC a cell in a host organism (comprising administering the novel composition
 CC which results in an anti-tumour, adjuvant, anti-viral or antagonised
 CC allergic effect), administering the IL-12 p40/IL-B30 antagonist resulting
 CC in amelioration of an autoimmune condition or a chronic inflammatory
 CC condition, increasing secretion of a primate IL-B30 (comprising
 CC expressing IL-B30 with IL-12 p40 or increasing secretion of IL-12 p40
 CC comprising expressing IL-12 p40 with IL-B30), screening for a receptor
 CC which binds the novel composition, modulating the inflammatory response
 CC in an animal and inducing the proliferation of memory T-cells by
 CC administering IL-B30 or its agonist. The invention is useful in
 CC forensics, research and teaching. They are useful to treat conditions
 CC associated with abnormal physiology including inflammatory conditions.
 CC Particularly the complex is useful to enhance anti-tumour, anti-viral and
 CC vaccine responses and to antagonise allergic responses. Antagonists may
 CC be useful to treat autoimmune diseases such as multiple sclerosis or
 CC psoriasis or chronic inflammatory conditions such as rheumatoid arthritis
 CC or inflammatory bowel disease. The present sequence represents human IL-
 CC B30.

XX Sequence 189 AA;

Query Match 100.0%; Score 189; DB 7; Length 189;

Best Local Similarity 100.0%; Pred. No. 1.4e-172; Indels 0; Gaps 0;

Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGSAVMLLLPMTAQGRAVPGSSPAWTCQQLSQKLTAWSAHPLVGHMDLREG 60

DB 1 MLGSAVMLLLPMTAQGRAVPGSSPAWTCQQLSQKLTAWSAHPLVGHMDLREG 60

QY 61 DEETNDVPHICGDCDQGLRDNSQFCQRIHQGLIFYEKLGSDIFTGSPSLPDS 120

DB 61 DEETNDVPHICGDCDQGLRDNSQFCQRIHQGLIFYEKLGSDIFTGSPSLPDS 120

QY 121 VAQLHASLGLSOLLQPEGHWHWTQIPLSPSPQWQRLRLFKILRSLOAFVAVARVF 180

DB 121 VAQLHASLGLSOLLQPEGHWHWTQIPLSPSPQWQRLRLFKILRSLOAFVAVARVF 180

QY 181 AHGAATLSP 189

DB 181 AHGAATLSP 189

RESULT 8

ID ADF70612 standard; protein; 189 AA.

XX ADF70612;

DT 07-OCT-2004 (first entry)

XX Human interleukin-19 protein.

KW Wound healing; agonist; antagonist; interleukin-23; IL-23; vulnary;
 KW cytokine; human; interleukin-19; IL-19.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..21 "Signal peptide"

XX Protein 22..189

XX /note= "Mature protein"

XX WO2004058178-A2.

```

XX PD 15-JUL-2004.
XX PF 18-DEC-2003; 2003WO-US040937.
XX PF 23-DEC-2002; 2002US-0436274P.
XX PR (SCHE ) SCHERING CORP.
XX PA Bowman EP, Chen S, Cua DJ;
XX PI WPI; 2004-525781/50.
XX DR N-PSDB; ADQ14468.
XX PT Treating inflammatory skin disorders or improving wound healing comprises
XX PT administering to a subject an agonist or antagonist of Interleukin-23.
XX PS Example; SEQ ID NO 4; 52pp; English.
XX CC The invention relates to a novel method for treating or improving wound
XX CC healing. The method comprises administering to a subject an agonist or
XX CC antagonist of interleukin (IL)-23. The invention further comprises: an
XX CC antagonist of IL-23 derived from the binding site of an antibody that
XX CC specifically binds to an IL-23 receptor; and a kit comprising the agonist
XX CC and a compartment or instructions for use or disposal. The interleukin-23
XX CC agents have vulnerary activity. The method is useful for treating or
XX CC improving wound healing. This sequence represents a cytokine human
XX CC interleukin-19 protein used in the wound healing method of the invention.
XX SQ Sequence 189 AA;
XX Query Match 100.0%; Score 189; DB 8; Length 189;
XX Best Local Similarity 100.0%; Pred. No. 1.4e-172;
XX Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLGSRAVMLLLLLPWTAGRAVPGSSPAWTCQOOLSQKLTAWSAHPLVGHMDLREEG 60
Db 1 MLGSRAVMLLLLLPWTAGRAVPGSSPAWTCQOOLSQKLTAWSAHPLVGHMDLREEG 60
Qy 61 DEETNDVPHIQCGDGDPOGLRDNQFCLQRIHQGLIFYEKLIGSDIFTGEPSSLDPSP 120
Db 61 DEETNDVPHIQCGDGDPOGLRDNQFCLQRIHQGLIFYEKLIGSDIFTGEPSSLDPSP 120
Qy 121 VAQLHASLLGLSLLQLOPEGHHWETQIIPSLSPSPQWQRLRLKILRSLOAFVAAARVF 180
Db 121 VAQLHASLLGLSLLQLOPEGHHWETQIIPSLSPSPQWQRLRLKILRSLOAFVAAARVF 180
Qy 181 AHGAATLSP 189
Db 181 AHGAATLSP 189
XX RESULT 9
XX ADS73601
XX ID ADS73601 standard; protein; 189 AA.
XX AC ADS73601;
XX XX
XX DT 16-DEC-2004 (first entry)
XX XX Human IL-23p19.
XX DE human; interleukin 23; subunit p19; IL-23; IL-23p19; tumour; growth;
XX KW agonist; antagonist; receptor; cancer; antigen-binding site; antibody;
XX KW extracellular region; antisense nucleic acid; small interference RNA;
XX KW siRNA; polyclonal; monoclonal; humanized; Fab; Fv; F(ab')2;
XX KW peptide mimetic; colon; ovarian; breast; melanoma; cachexia; anorexia;
XX KW angiogenesis; gastrointestinal tract; respiratory tract;
XX KW reproductive system; endocrine system.
XX OS Homo sapiens.
XX XX
XX FH Key Location/Qualifiers

```

Peptide 1. .21
/note= "Signal peptide"
Protein 22. .189
/note= "Mature IL-23p19"

WO2004081190-A2.
23-SEP-2004.
09-MAR-2004; 2004WO-US007198.
10-MAR-2003; 2003US-0453672P.
(SCHE) SCHERING CORP.
Oft M, Mcclanahan TK;
WPI; 2004-668951/65.
N-PSDB; ADS73600.

Modulating tumor growth, useful for treating a subject suffering from cancer or tumor, comprises contacting a tumor cell with an agonist or antagonist of IL-23.

Claim 4; SEQ ID NO 2; 57pp; English.

This sequence represents human interleukin 23 subunit p19 (IL-23p19). The method of the invention for modulating tumor growth comprises contacting a tumor cell with an agonist or antagonist of IL-23. The agonist or antagonist is a binding composition which specifically binds the IL-23 p19 subunit or the IL-23 receptor (IL-23R) protein. The identified agonist or antagonist may be used for diagnosing or treating a subject suffering from a cancer or tumor. The binding composition comprises an antigen-binding site of the antibody, an extracellular region of IL-23R, a small molecule, an antisense nucleic acid or small interference RNA (siRNA), or a detectable label. The binding composition comprises a polyclonal antibody, a monoclonal antibody, a humanized antibody or its fragment, a Fab, Fv, F(ab') 2 fragment, or a peptide mimetic of an antibody. The tumor cell is a colon, ovarian or breast cancer cell, or melanoma cell. In the treatment method, the antagonist of IL-23 inhibits growth of cancer or tumor, cachexia, anorexia or angiogenesis. The cancer of tumor is of the gastrointestinal tract, respiratory tract, reproductive system or endocrine system. In diagnosing cancer or tumor, the binding composition comprises a nucleic acid probe or primer that specifically binds or hybridises to human or mouse IL-23p19 cDNA sequences, or the human IL-23R sequence.

Query Match 100.0%; Score 189; DB 8; Length 189;
Best Local Similarity 100.0%; Pred. No. 1.4e-172;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MLGSRAVMLLLLLPWTAGRAVPGSSPAWTCQOOLSQKLTAWSAHPLVGHMDLREEG 60
1 MLGSRAVMLLLLLPWTAGRAVPGSSPAWTCQOOLSQKLTAWSAHPLVGHMDLREEG 60
61 DEETNDVPHIQCGDGDPOGLRDNQFCLQRIHQGLIFYEKLIGSDIFTGEPSSLDPSP 120
61 DEETNDVPHIQCGDGDPOGLRDNQFCLQRIHQGLIFYEKLIGSDIFTGEPSSLDPSP 120
121 VAQLHASLLGLSLLQLOPEGHHWETQIIPSLSPSPQWQRLRLKILRSLOAFVAAARVF 180
121 VAQLHASLLGLSLLQLOPEGHHWETQIIPSLSPSPQWQRLRLKILRSLOAFVAAARVF 180
181 AHGAATLSP 189
181 AHGAATLSP 189

RESULT 10
ADV98151
ID ADV98151 standard; protein; 189 AA.

XX ADV98151;
AC 10-MAR-2005 (first entry)
XX
DT
XX
DE Novel human interleukin B30 protein.
XX
KW DNA purification; cytokine; interleukin-B30; IL-B30; inflammation;
KW autoimmune disorder; forensic science; differential expression.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT Protein /note= "signal peptide"
FT 22..189
FT /note= "mature IL-B30 protein"
XX
XX US6835825-B1.
XX 28-DEC-2004.
XX
XX 25-APR-2000; 2000US-00558474.
XX
XX 25-JUL-1997; 97US-0053765P.
XX 24-JUL-1998; 98US-00122443.
XX
XX (SCHE) SCHERING CORP.
XX
XX Bazan JF;
XX
XX WPI: 2005-077885/09.
XX N-PSDB; ADV98150, ADV98152.
XX
XX Detecting interleukin-B30 polynucleotide, comprises contacting
PT polynucleotide with probe capable of hybridizing with contiguous
PT nucleotides of polynucleotide to form duplex, where detection of duplex
PT indicates presence of polynucleotide.
XX
XX Disclosure; SEQ ID NO 2; 32pp; English.
XX
XX The invention relates to a method of detecting (M1) a polynucleotide, by
CC contacting a polynucleotide with a probe (PB) that hybridizes, under
CC stringent wash conditions to at least 394 or 25 contiguous nucleotides of
CC open reading frame of a fully defined interleukin (IL)-B30 sequence of
CC 570 (S1) or 1203 (S2) base pairs, to form duplex, where detection of
CC duplex indicates presence of polynucleotide. The method is useful for
CC detecting IL-B30 polynucleotide. The method is useful for detecting the
CC expression of IL-B30 polynucleotide, and for detecting levels of IL-B30
CC in samples from patient suspected of having abnormal conditions such as
CC inflammatory or autoimmune. The method is also useful in forensic
CC science, e.g. to distinguish rodent from human or to distinguish between
CC different cell exhibiting differential expression or modification
CC patterns. The method is further useful for detecting disease or disorder
CC associated with abnormal expression or signaling by IL-B30. This sequence
CC corresponds to the novel interleukin-B30 protein.
XX
XX Sequence 189 AA;
SQ

Query Match 100.0%; Score 189; DB 9; Length 189;
Best Local Similarity 100.0%; Pred. No. 1.4e-172;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRAVMLLLPMTAAGRAVPGSSPAWTCQQLSQKLCCTLAWSAHLVGHMDLREEG 60
DB 1 MLGRAVMLLLPMTAAGRAVPGSSPAWTCQQLSQKLCCTLAWSAHLVGHMDLREEG 60
QY 61 DEETNDVPHICGGDCDQGLRDNQSQCLQRIHQGLIFYEKLGSDFITGSPSLPDSF 120
DB 61 DEETNDVPHICGGDCDQGLRDNQSQCLQRIHQGLIFYEKLGSDFITGSPSLPDSF 120
QY 121 VAQLHASLLGLSQLLQPEGHWHWETQOIPSLSPSQPWORLLRFLKILRSIQAFVAVARVF 180
DB

DB 121 VAQLHASLLGLSQLLQPEGHWHWETQOIPSLSPSQPWORLLRFLKILRSIQAFVAVARVF 180
QY 181 AHGAATLSP 189
DB 181 AHGAATLSP 189
RESULT 11
AEA51094
ID AEA51094 standard; protein; 189 AA.
XX
XX AEA51094;
XX
XX 11-AUG-2005 (first entry)
XX Human p19 protein.
XX
XX Diagnosis; therapeutic; asthma; antiasthmatic; immune disorder;
KW inflammation; respiratory disease; allergy; anti-allergic;
KW chronic obstructive pulmonary disease; respiratory-gen.;
KW pulmonary fibrosis; antiinflammatory; pneumonia; infection; p19 protein.
XX
XX Homo sapiens.
XX OS
XX WO2005052157-A1.
XX
XX 09-JUN-2005.
XX
XX 18-NOV-2004; 2004WO-US038886.
XX
XX 21-NOV-2003; 2003US-00720026.
XX
XX (SCHE) SCHERING CORP.
XX
XX Chirica M, Kastelein RA, Moore KW, Parham CL;
XX WPI: 2005-418000/42.
XX N-PSDB; AEA51093.
XX
XX Use of an agonist or antagonist of DNAX cytokine receptor subunit 5
PT (DCRS5) or of p19 for treating a human subject experiencing a
PT physiological disorder such as allergy or chronic obstructive pulmonary
PT disorder (COPD).
XX
XX Claim 1; SEQ ID NO 6; 89pp; English.
XX
XX The present invention relates to a method of treating a human subject
CC experiencing a physiological disorder. The method involves administering
CC an agonist or antagonist of DNAX cytokine receptor subunit 5 (DCRS5, also
CC known as IL-23R) or of p19, where the disorder comprises asthma or
CC allergy, chronic obstructive pulmonary disorder (COPD) or an interstitial
CC lung disorder. The invention is useful for treating interstitial lung
CC disorder e.g. idiopathic pulmonary fibrosis, eosinophilic granuloma and
CC hypersensitivity pneumonitis. The present sequence is the human p19
CC protein.
XX
XX Sequence 189 AA;
SQ

Query Match 100.0%; Score 189; DB 9; Length 189;
Best Local Similarity 100.0%; Pred. No. 1.4e-172;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRAVMLLLPMTAAGRAVPGSSPAWTCQQLSQKLCCTLAWSAHLVGHMDLREEG 60
DB 1 MLGRAVMLLLPMTAAGRAVPGSSPAWTCQQLSQKLCCTLAWSAHLVGHMDLREEG 60
QY 61 DEETNDVPHICGGDCDQGLRDNQSQCLQRIHQGLIFYEKLGSDFITGSPSLPDSF 120
DB 61 DEETNDVPHICGGDCDQGLRDNQSQCLQRIHQGLIFYEKLGSDFITGSPSLPDSF 120
QY 121 VAQLHASLLGLSQLLQPEGHWHWETQOIPSLSPSQPWORLLRFLKILRSIQAFVAVARVF 180
DB 121 VAQLHASLLGLSQLLQPEGHWHWETQOIPSLSPSQPWORLLRFLKILRSIQAFVAVARVF 180

AA161618 to AA161697 encode the human secreted proteins given in AY948998 to AY949980, isolated from human adult brain, adult thyroid, adult retina, foetal carcinoma, adult blood, adult neural, foetal kidney, adult placenta, adult testis, whole embryo, adult cartilage, kidney, foetal brain, adult thymus, foetal placenta, adult uterus, adult tumour, and adult bladder. cDNA libraries. The polynucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. The polynucleotides can be used as markers for tissues in which the protein is preferentially expressed, as molecular weight markers on Southern gels, and as chromosome markers or tags to identify chromosomes or to map gene positions. The proteins can be used in the treatment of

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2006, 04:52:34 ; Search time 24.5455 Seconds
(without alignments)
740.869 Million cell updates/sec

Title: US-10-797-157-2
Perfect score: 189
Sequence: 1 MLGSRVNMILLLEPWAQGR.....QAFVAVARVFAGHAATLSP 189

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 1

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_80.*

- 1: pir1.*
- 2: pir2.*
- 3: pir3.*
- 4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	4.2	232	2 G82842	DNA repair protein
2	8	4.2	299	2 T29226	hypothetical prote
3	8	4.2	313	2 A82640	transcription regu
4	8	4.2	391	2 T40169	hypothetical prote
5	7	3.7	136	2 B95333	hypothetical prote
6	7	3.7	151	2 AB1275	hypothetical prote
7	7	3.7	151	2 AB1638	hypothetical prote
8	7	3.7	164	2 S18038	homeotic protein S
9	7	3.7	189	1 LPHUD	apolipoprotein D p
10	7	3.7	192	2 AE0043	probable membrane
11	7	3.7	209	2 D86758	orotate phosphorib
12	7	3.7	214	2 A83416	hypothetical prote
13	7	3.7	235	2 A95603	hypothetical prote
14	7	3.7	238	2 A72374	hypothetical prote
15	7	3.7	248	2 T44932	3-oxoacyl-lacyl-ca
16	7	3.7	254	2 JQ0490	regulatory protein
17	7	3.7	260	2 F82120	zinc ABC transport
18	7	3.7	273	1 ED8E12	immediate-early pr
19	7	3.7	284	2 T42608	immediate-early pr
20	7	3.7	307	2 C70952	probable suga prot
21	7	3.7	333	2 A96829	probable RING fing
22	7	3.7	339	1 KHM5B	cathepsin B (EC 3.
23	7	3.7	339	1 KHRTB	cathepsin B (EC 3.
24	7	3.7	349	2 T42965	glycoprotein - ate
25	7	3.7	376	2 B41870	DNA-directed DNA p
26	7	3.7	391	2 T24813	hypothetical prote
27	7	3.7	393	1 A48573	calreticulin autoa
28	7	3.7	396	2 B70394	ABC transporter -
29	7	3.7	413	2 T49545	hypothetical prote

ALIGNMENTS

RESULT 1

G82842

DNA repair protein XF0148 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000

C:Accession: G82842

R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: G82842

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-232 <SIM>

A:Cross-references: UNIPARC:UPI0000165A4C; GB:AE003868; GB:AE003849; NID:g9104930; PIDN

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Carrer, i

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, i

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohu

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, C.Y.

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; de Oliveira, R.C.; Palmieri, D.

M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

C:Gene: XF0148

C:Superfamily: DNA repair protein radc

Query Match 4.2% Score 8; DB 2; Length 232;

Best Local Similarity 100.0%; Pred.No.6.5; Mismatches 0; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 AHGAATLS 188

Db 26 AHGAATLS 33

RESULT 2

T29226

hypothetical protein F55G1.9 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T29226

R:Murray, J.; Le, T.T.

submitted to the EMBL Data Library, May 1996

A;Description: The sequence of C. elegans cosmid F55G1.

A;Reference number: 220591

A;Accession: T29226

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-299 <MUR>

A;Cross-references: UNIPROT:Q20848; UNIPARC:UPI00001322F4; EMBL:U58750; PIDN:AAB00645.1;

A;Experimental source: strain Bristol N2; clone F55G1

C;Genetics:

A;Gene: CESP:F55G1.9

A;Map position: 4

A;Introns: 37/1; 121/3

C;Superfamily: pyroline-5-carboxylate reductase

Query Match	4.2%;	Score 8;	DB 2;	Length 299;
Best Local Similarity	100.0%;	Pred. No. 8.1;		
Matches	8;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;

Qy 24 GGSSPAWT 31

Db 192 GGSSPAWT 199

|||||

RESULT 3

A82640

C;Description: transcription regulator lysR family XF1768 [imported] - Xylella fastidiosa (strain 9a5C)

C;Species: Xylella fastidiosa

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Accession: A82640

R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing

Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Reference number: A82515; MUID:20365717; PMID:10910347

A;Note: for a complete list of authors see reference number A59328 below

A;Accession: A82640

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-313 <STM>

A;Cross-references: UNIPROT:Q9PCL0; UNIPARC:UPI000000C2819; GB:A8003999; GB:A8003849; NID

A;Experimental source: strain 9a5C

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Camargo, D.M.; Carrer, H

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B

A;Authors: Martins, E.M.P.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tshuko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A;Reference number: A59328

A;Contents: annotation

C;Genetics:

A;Gene: XF1768

C;Superfamily: hypothetical protein b1328

Query Match	4.2%;	Score 8;	DB 2;	Length 313;
Best Local Similarity	100.0%;	Pred. No. 8.4;		
Matches	8;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;

Qy 169 LQAFVA 176

Db 26 LQAFVA 33

|||||

RESULT 4

T40169

C;Description: hypothetical protein SPBC30B4.03c - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: T40169

R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Duesterhoeft, A.
submitted to the EMBL Data Library, August 1998

A;Reference number: Z21909

A;Accession: T40169

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-391 <LYN>

A;Cross-references: UNIPROT:O74364; UNIPARC:UPI00000698E3; EMBL:AL031262; PIDN:CAA20316.

A;Experimental source: strain 972h-; cosmid c30B4

C;Genetics:

A;Gene: SPDB:SPBC30B4.03c

A;Map position: 2

Query Match	4.2%;	Score 8;	DB 2;	Length 391;
Best Local Similarity	100.0%;	Pred. No. 10;		
Matches	8;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;

Qy 114 SLLPDSPV 121

Db 211 SLLPDSPV 218

|||||

RESULT 5

B95333

C;Description: hypothetical protein Sma1053 [imported] - Sinorhizobium meliloti (strain 1021) megaplasm

C;Species: Sinorhizobium meliloti

C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

C;Accession: B95333

R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows

; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.

Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot

A;Reference number: A95262; MUID:21396509; PMID:11481432

A;Accession: B95333

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-136 <KUR>

A;Cross-references: UNIPROT:Q92ZC0; UNIPARC:UPI000000CB12D; GB:A8006469; PIDN:AAK65228.1;

A;Experimental source: strain 1021, megaplasmid pSymA

R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,

pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,

hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.

A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A;Reference number: A96039; MUID:21368234; PMID:11474104

A;Contents: annotation

C;Genetics:

A;Gene: Sma1053

A;Genome: plasmid

Query Match	3.7%;	Score 7;	DB 2;	Length 136;
Best Local Similarity	100.0%;	Pred. No. 38;		
Matches	7;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;

Qy 6 AVMLLL 12

Db 18 AVMLLL 24

|||||

RESULT 6

AB1275

C;Description: hypothetical protein lmo1602 [imported] - Listeria monocytogenes (strain EGD-e)

C;Species: Listeria monocytogenes

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C;Accession: AB1275

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker

; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauguet, O.; Entian, K.D.; Feih, H.

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma

ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A:Title: Comparative genomics of *Listeria* species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AB1275
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-151 <GLA>
A:Cross-references: UNIPROT:Q8YGT1; UNIPARC:UPI0000055247; GB:NC_003210; PIDN:CAC99680.1
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo1602

Query Match 3.7%; Score 7; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 127 SLLGLSQ 133
|||||
Db 89 SLLGLSQ 95

RESULT 7
AB1638
Hypothetical protein homolog lin1643 [imported] - *Listeria innocua* (strain Clip11262)
C:Species: *Listeria innocua*
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AB1638
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Makok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AB1638
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-151 <GLA>
A:Cross-references: UNIPROT:Q92BA7; UNIPARC:UPI000000CC5FF; GB:AL592022; PIDN:CAC96874.1;
A:Experimental source: strain Clip11262
C:Genetics:
A:Gene: lin1643

Query Match 3.7%; Score 7; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 127 SLLGLSQ 133
|||||
Db 89 SLLGLSQ 95

RESULT 8
S18038
homeotic protein S8 - mouse (fragment)
C:Species: *Mus musculus* (house mouse)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-Oct-2004
C:Accession: I48410; S00990; S18038
R:Opateiten, D.J.; Vogels, R.; Robert, B.; Kalkhoven, E.; Zwartkruis, F.; de Laaf, L.; D Mech. Dev. 34, 29-41, 1991
A:Title: The mouse homeobox gene, S8, is expressed during embryogenesis predominantly in
A:Reference number: I48410; MUID:92001534; PMID:1680375
A:Accession: I48410
A>Status: preliminary; translated from GB/EMBL/DBJ.
A:Molecule type: mRNA
A:Residues: 1-164 <RES>
A:Cross-references: UNIPROT:Q06348; UNIPARC:UPI000017A2BC; EMBL:X52875; NID:G51365; PID:
R.Kongswan, K.; Webb, E.; Housiaux, P.; Adams, J.M.
EMBO J. 7, 2131-2138, 1988
A:Title: Expression of multiple homeobox genes within diverse mammalian haemopoietic lin
A:Reference number: S00987; MUID:88329001; PMID:2901346
A:Accession: S00990
A:Molecule type: mRNA

A:Residues: 50-74 <KON>
A:Cross-references: UNIPARC:UPI000017A2BD; EMBL:X14572
C:Genetics:
A:Gene: S8
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:16-72/Domain: homeobox homology <Hox>

Query Match 3.7%; Score 7; DB 2; Length 164;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 PGSSSPA 29
|||||
Db 127 PGSSSPA 133

RESULT 9
LPHUD
apolipoprotein D precursor [validated] - human
N:Alternate names: apod; gross cystic disease fluid protein 24 (GCDFF-24)
C:Species: *Homo sapiens* (man)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C:Accession: A26958; A03224; S13050
R:Drayna, D.T.; McLean, J.W.; Wion, K.L.; Trent, J.M.; Drabkin, H.A.; Lawn, R.M.
DNA 6, 199-204, 1987
A:Title: Human apolipoprotein D gene: gene sequence, chromosome localization, and homolo
A:Reference number: A26958; MUID:87246069; PMID:2439269
A:Accession: A26958
A:Molecule type: DNA
A:Residues: 1-189 <DRA1>
R:Drayna, D.; Fielding, C.; McLean, J.; Baer, B.; Castro, G.; Chen, E.; Comstock, L.; He
J. Biol. Chem. 261, 16535-16539, 1986
A:Title: Cloning and expression of human apolipoprotein D cDNA.
A:Reference number: A03224; MUID:87057347; PMID:3453108
A:Accession: A03224
A:Molecule type: mRNA
A:Residues: 1-189 <DRA2>
A:Cross-references: UNIPARC:UPI00000369E0; GB:J02611; NID:G178840; PIDN:AAB59517.1; PID
A>Note: part of the sequence was confirmed by protein sequencing
R:Balbin, M.; Freije, J.M.P.; Fuyo, A.; Sanchez, L.M.; Lopez-Otin, C.
Biochem. J. 271, 803-807, 1990
A:Title: Apolipoprotein D is the major protein component in cyst fluid from women with h
A:Reference number: S13050; MUID:91059519; PMID:2244881
A:Accession: S13050
A:Molecule type: protein
A:Residues: 28-41; 42-45; X', 47-51; 52-60; 61-64, X', 66-73; 76-82; 83-97, X', 99-104; 109-110, X'
A:Cross-references: UNIPARC:UPI0000040C85; UNIPARC:UPI0000040CD2; UNIPARC:UPI0000040CD3;
3E2; UNIPARC:UPI00001743E3; UNIPARC:UPI00001743E4; UNIPARC:UPI00001743E5
A:Experimental source: mammary cyst fluid
A>Note: carbohydrate binding sites determined; the sequence of the amino-terminal pyrogl
R:Peitsch, M.C.; Boguski, M.S.
submitted to the Brookhaven Protein Data Bank, April 1992
A:Reference number: A50026; PDB:2APD
A:Contents: annotation; theoretical model, residues 21-189
R:Yang, C.Y.; Gu, Z.W.; Blanco-Vaca, F.; Gaskell, S.J.; Yang, M.; Massey, J.B.; Gotto Jr
Biochemistry 33, 12451-12455, 1994
A:Title: Structure of human apolipoprotein D: locations of the intermolecular and intran
A:Reference number: A55901; MUID:95001965; PMID:7918467
A:Contents: annotation; confirmation of peptide sequence overlap; disulfide bonds; N-gly
R:Schindler, P.A.; Settineri, C.A.; Collet, X.; Fielding, C.J.; Burlingame, A.L.
Protein Sci. 4, 791-803, 1995
A:Title: Site-specific detection and structural characterization of the glycosylation of
pectrometry and sequential glycosidase digestion.
A:Reference number: A57914; MUID:95338133; PMID:7613477
A:Contents: annotation; N-glycosylation
C:Comment: Apod occurs in the macromolecular complex with lecithin-cholesterol acyltran
C:Comment: Apod is primarily localized in HDL (60-65%), with most of the remainder in Vi
C:Comment: Apod has been found in liver, intestine, pancreas, kidney, placenta, adrenal,
C:Genetics:
A:Gene: GDB:APOD
A:Cross-references: GDB:119690; OMIM:107740
A:Map position: 3q27-3qter

A;Introns: 41/3; 82/2; 112/1
A;Note: the first intron occurs before the initiator codon
C;Superfamily: lipocalin; lipocalin homology
C;Keywords: glycoprotein; lipid binding; lipid transport; lipoprotein; plasma; pyroglutamate
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-189/Product: apolipoprotein D #status experimental <MAT>
F;37-185/Domain: lipocalin homology <LIP>
F;21/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental
F;28-134,61-185/disulfide bonds: #status experimental
F;65,98/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;136/disulfide bonds: interchain (to apolipoprotein A-II 29) #status experimental

Query Match 3.7%; Score 7; DB 1; Length 189;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 VMLLLLL 13
|||||
Db 2 VMLLLLL 8

RESULT 10
AE0043
probable membrane protein YPO0349 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AE0043
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Lil, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AE0043
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-192 <KUR>
A;Cross-references: UNIPROT:Q8ZIIY5; UNIPARC:UPI000000CD6AC; GB:AL590842; PIDN:CAC89208.1;
C;Genetics:
A;Gene: YPO0349
C;Superfamily: Escherichia coli hypothetical protein b4140

Query Match 3.7%; Score 7; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LLLLLPW 15
|||||
Db 97 LLLLLPW 103

RESULT 11
D86758
orotate phosphoribosyltransferase (EC 2.4.2.10) [imported] - Lactococcus lactis subsp. 1
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: D86758
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissbach, J.; Ehrlich Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis subsp. 1
A;Reference number: A86625; MUID:21235186; PMID:11133741
A;Accession: D86758
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-209 <STO>
A;Cross-references: UNIPROT:Q9CGM8; UNIPARC:UPI0000132CB; GB:AE005176; PID:g12724022; F
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: pyrE
C;Superfamily: orotate phosphoribosyltransferase; orotate phosphoribosyltransferase homolog
C;Keywords: glycosyltransferase; pentosyltransferase

Query Match 3.7%; Score 7; DB 2; Length 209;

Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 SLSPSQP 155
|||||
Db 18 SLSPSQP 24

RESULT 12
A83416
hypothetical protein PA1825 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: A83416
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83416
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-214 <STO>
A;Cross-references: UNIPROT:Q9I2S0; UNIPARC:UPI000000C54B5; GB:AE004609; GB:AE004091; NID
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA1825

Query Match 3.7%; Score 7; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 AFVAVAA 177
|||||
Db 42 AFVAVAA 48

RESULT 13
A99603
hypothetical protein MYPV 7290 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: A99603
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis
A;Reference number: A99512; MUID:21267165; PMID:111353084
A;Accession: A99603
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-235 <KUR>
A;Cross-references: UNIPROT:Q98PU3; UNIPARC:UPI000000C80FF; GB:AL445566; PID:g14090144; P
A;Experimental source: strain UAB CTIP
C;Genetics:
A;Gene: MYPV 7290
A;Genetic code: SGC3

Query Match 3.7%; Score 7; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 SLGLSQ 133
|||||
Db 16 SLGLSQ 22

RESULT 14
A72374
hypothetical protein TM0465 - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: A72374

R; Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.

Nature 399, 323-329, 1999
 A; Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequencing
 A; Reference number: A72200; MUID:99287316; PMID:10360571
 A; Accession: A72374
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-238 <ARN>
 A; Cross-references: UNIPROT:Q9WY76; UNIPARC:UPI00000C1415; GB:AE001724; GB:AE000512; NID
 A; Experimental source: strain MSB8
 C; Genetics:
 A; Gene: TM0465
 C; Superfamily: Thermotoga maritima hypothetical protein TM0465

Query Match 3.7%; Score 7; DB 2; Length 238;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 111 GEPSSLIP 117
 |||||
 Db 55 GEPSSLIP 61

RESULT 15
 T44932
 3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) [imported] - Agrobacterium tumefaciens
 C; Species: Agrobacterium tumefaciens
 C; Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 05-Oct-2004
 C; Accession: T44932
 R; Kim, K.S.; Farrand, S.K.
 J. Bacteriol. 178, 3275-3284, 1996
 A; Title: Ti plasmid-encoded genes responsible for catabolism of the crown gall opine man by the plant tumor.
 A; Reference number: Z22872; MUID:96236046; PMID:8655509
 A; Accession: T44932
 A; Status: preliminary; translated from GB/EMBL/DBJ
 A; Molecule type: DNA
 A; Residues: 1-248 <KIM>
 A; Cross-references: UNIPROT:Q44326; UNIPARC:UPI00000B1373; EMBL:U19620; NID:g797330; PID
 A; Experimental source: strain 15955
 C; Genetics:
 A; Gene: mocc
 A; Genome: plasmid pTi15955
 C; Superfamily: short-chain dehydrogenase; short-chain alcohol dehydrogenase homology
 C; Keywords: oxidoreductase

Query Match 3.7%; Score 7; DB 2; Length 248;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 132 SOLLQPE 138
 |||||
 Db 201 SOLLQPE 207

Search completed: June 20, 2006, 04:59:43
 Job time : 27.5455 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2006, 04:47:24 ; Search time 191.945 Seconds
(without alignments)
910.821 Million cell updates/sec

Title: US-10-797-157-2

Perfect score: 189

Sequence: 1 MLGSRVAVMLLLPWTAGQR.....QAFVAVARVFAHGAATLSP 189

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2849598 seqs, 925015592 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	189	100.0	189	2	Q9H2A5 HUMAN
2	121	64.0	189	2	Q6NZ80 HUMAN
3	121	64.0	189	2	Q6NZ82 HUMAN
4	121	64.0	189	2	Q9NPF7 HUMAN
5	31	16.4	185	2	Q2Q586 FELCA
6	25	13.2	193	2	Q9N2H9 PIG
7	24	12.7	192	2	Q64FUI HORSE
8	20	10.6	189	2	Q6LA37 CAVPO
9	16	8.5	196	2	Q9I284 RAT
10	14	7.4	184	2	Q8OWE2 PERMA
11	12	6.3	196	2	Q9EQ14 MOUSE
12	9	4.8	151	2	Q4V817 XENLA
13	9	4.8	538	2	Q4KJ01 PSEF5
14	8	4.2	102	2	Q6TM10 DROME
15	8	4.2	129	2	Q4S5N0 TETNG
16	8	4.2	224	1	RADC_XYLFA
17	8	4.2	224	1	RADC_XYLFT
18	8	4.2	242	2	Q3R181_XYLFA
19	8	4.2	242	2	Q3REA4_XYLFA
20	8	4.2	261	2	Q5S6M3_VIBF1
21	8	4.2	286	2	Q397K3_BURS3
22	8	4.2	299	1	P5CR_CABEL
23	8	4.2	301	2	Q98J00_RHILO
24	8	4.2	303	2	Q3GX45_9ACTO
25	8	4.2	311	2	Q3YJ61_SHPU
26	8	4.2	313	2	Q9PCL0_XYLFA
27	8	4.2	391	2	O74364_SCHPO
28	8	4.2	399	2	Q3P0W7_9GAMM
29	8	4.2	399	2	Q8JNA4_FPVIL
30	8	4.2	463	2	Q5A927_CANAL
31	8	4.2	509	2	Q3QEB3_9GAMM

32	8	4.2	512	1	GATA_BORBR	Q7wev1 bordetella
33	8	4.2	512	1	GATA_BORPA	Q7w3h7 bordetella
34	8	4.2	522	2	Q6GPA5_XENLA	Q6gpa5 xenopus lae
35	8	4.2	581	2	Q73ZW8_MYCPA	Q73zw8 mycobacteri
36	8	4.2	660	1	S39A4_MOUSE	Q781q7 mus musculu
37	8	4.2	672	2	Q3U263_MOUSE	Q3u263 m nod-deriv
38	8	4.2	787	2	Q44R46_CHLLI	Q44r46 chlorobium
39	8	4.2	986	2	Q4QAL9_LEIMA	Q4qal9 leishmania
40	8	4.2	2629	2	Q4Q905_LEIMA	Q4q905 leishmania
41	7	3.7	37	2	Q7KZ28_HUMAN	Q7kz28 homo sapien
42	7	3.7	44	2	Q14081_HUMAN	Q14081 homo sapien
43	7	3.7	54	2	Q4Y928_PLACH	Q4y928 plasmodium
44	7	3.7	80	2	Q4I9U8_GIBZE	Q4i9u8 gibberella
45	7	3.7	80	2	Q6ASQ3_ORYSA	Q6asq3 oryza sativ

ALIGNMENTS

RESULT 1

Q9H2A5 HUMAN

ID Q9H2A5_HUMAN PRELIMINARY; PRT; 189 AA.

AC Q9H2A5;

DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.

DT 01-MAR-2001, sequence version 1.

DT 07-FEB-2006, entry version 16.

DE Interleukin 23 p19 subunit.

GN Name=IL23A;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=20567322; PubMed=1114383; DOI=10.1016/S1074-7613(00)00070-4;

RA Oppmann B., Lesley R., Blom B., Timans J.C., Xu Y., Hunte B., Vega F., Yu N., Wang J., Singh K., Zonin F., Vaishberg E., Churakova T., Liu M.-R., Gorman D., Wagner J., Zurawski S., Liu Y.-J., Abrams J.S., Moore K.W., Rennick D., de Waal-Malefyt R., Hamum C., Bazan J.F., Kastelein R.A.;

RT "Novel p19 protein engages IL-12p40 to form a cytokine, IL-23, with biological activities similar as well as distinct from IL-12.";

RL Immunity 13:715-725(2000).

CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License

DR EMBL; AF301620; AAG37232.1; -; mRNA.

DR Ensembl; ENSG00000110944; Homo sapiens.

DR GO; GO:0005576; C:extracellular region; IEA.

DR GO; GO:0005125; F:cytokine activity; IEA.

DR GO; GO:0006955; P:immune response; IEA.

DR InterPro; IPR012351; Cytokine_4_hlx.

DR InterPro; IPR010831; IL23A.

DR InterPro; IPR003573; IL6 MGF GCSP.

DR PANTHER; PTHR15947; IL23A; 1.

DR Pfam; PF00489; IL6; 1.

SQ SEQUENCE 189 AA; 20744 MW; BFB5C0F42D4C1E3A CRC64;

Query Match 100.0%; Score 189; DB 2; Length 189;

Best Local Similarity 100.0%; Pred. No. 3.5e-171;

Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGSRVAVMLLLPWTAGRVPGSSPAWTCQQLSQKLCCTLAWSAHLVGHMDLRERG 60

DB 1 MLGSRVAVMLLLPWTAGRVPGSSPAWTCQQLSQKLCCTLAWSAHLVGHMDLRERG 60

QY 61 DEETNDVPHICGCGDPCQGLRDNDSQCILQRIHQGLIFYEKLGSDIFTGSPSLPDSF 120

DB 61 DEETNDVPHICGCGDPCQGLRDNDSQCILQRIHQGLIFYEKLGSDIFTGSPSLPDSF 120

QY 121 VAQLHASLLGLSQLQPEGHWTQOIFSLSPSQWQRLLLRFKILRSIAQVAVARVF 180

```
Db 121 VAQHASLGLSULQPEGHWHETQOIPSLSPSQWQRLILRFXILRSLOAFVAVARVF 180
Qy 181 AHGAATLSP 189
Db 181 AHGAATLSP 189

RESULT 2
Q6N280 HUMAN PRELIMINARY; PRT; 189 AA.
ID Q6N280
AC Q6N280
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Interleukin 23, alpha subunit p19,.
GN Name=IL23A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RA Director MGC Project;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC -----
DR EMBL; BC066269; AAH66269.1; -; mRNA.
DR Ensembl; ENSG00000110944; Homo sapiens.
DR HGNC; HGNC:15486; IL23A.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR010831; IL23A.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR PANTHER; PTHR15947; IL23A; 1.
DR Pfam; PF00489; IL6; 1.
SQ SEQUENCE 189 AA; 20718 MW; 594290F188EC1B9F CRC64;

Query Match 64.0%; Score 121; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 1.9e-106;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLGSRAVMLLLPWTAGRAVFGSGSPAWTQCQQLSLAWSAPLVGHMDLREEG 60
```

```
Db 1 MLGSRAVMLLLPWTAGRAVFGSGSPAWTQCQQLSLAWSAPLVGHMDLREEG 60
Qy 61 DEETTNDVPHIQCGDCDPOGLRDNSQFCLQRHQGLIFYEKLIGSIFDFTGEPSSLDPSP 120
Db 61 DEETTNDVPHIQCGDCDPOGLRDNSQFCLQRHQGLIFYEKLIGSIFDFTGEPSSLDPSP 120
Qy 121 V 121
Db 121 V 121

RESULT 3
Q6N282 HUMAN PRELIMINARY; PRT; 189 AA.
ID Q6N282
AC Q6N282
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Interleukin 23, alpha subunit p19,.
GN Name=IL23A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RA Director MGC Project;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC -----
DR EMBL; BC066267; AAH66267.1; -; mRNA.
DR Ensembl; ENSG00000110944; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR010831; IL23A.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR PANTHER; PTHR15947; IL23A; 1.
DR Pfam; PF00489; IL6; 1.
SQ SEQUENCE 189 AA; 20775 MW; 51B5C5B49CADCI4F CRC64;

Query Match 64.0%; Score 121; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 1.9e-106;
```

Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLGRAVMLLLPWTAGRAVPGSSPAWTCQQLSQKLTCLAWSAPLVGHMDLREEG 60
Db 1 MLGRAVMLLLPWTAGRAVPGSSPAWTCQQLSQKLTCLAWSAPLVGHMDLREEG 60
Qy 61 DEETNDVPHIQCGDGPQGLRDNSQFCLQRIHQGLIFYEKLIGSDIFTGEPSPLLPSP 120
Db 61 DEETNDVPHIQCGDGPQGLRDNSQFCLQRIHQGLIFYEKLIGSDIFTGEPSPLLPSP 120
Qy 121 V 121
Db 121 V 121

RESULT 4
Q9NPF7 HUMAN PRELIMINARY; PRT; 189 AA.
AC Q9NPF7
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE SGRF precursor (IL-23 p19) (Interleukin 23, alpha subunit p19).
GN Name=SGRF; Synonyms=IL23A; ORFNames=UNQ2498;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN 1
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Splice;
RA Hirata Y., Kosegawa Y.;
RT "SGRF; a novel member of the IL-6/G-CSF family.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Curlew C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA Sehgiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R.L., Watanabe C., Weland D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment";
RL Genome Res. 13:2265-2270(2003).
[3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[4]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RA Director MGC Project;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
[5]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RA Strausberg R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License

DR EMBL; AB030000; BAA93686.1; -; mRNA.
DR EMBL; AY359083; AAQ89442.1; -; mRNA.
DR EMBL; BC066268; AAH66268.1; -; mRNA.
DR EMBL; BC067511; AAH67511.1; -; mRNA.
DR EMBL; BC067512; AAH67512.1; -; mRNA.
DR EMBL; BC067513; AAH67513.1; -; mRNA.
DR EMBL; AB030001; BAA93687.1; -; Genomic DNA.
DR Ensembl; ENSG00000110944; Homo sapiens.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR010831; IL23A.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR PANTHER; PTHR15947; IL23A; 1.
DR Pfam; PF00489; IL6; 1.
DR Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 189 SGRF.
SQ SEQUENCE 189 AA; 20730 MW; 51B5C0F188EC1B9F CRC64;
Query Match 64.0%; Score 121; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 1.9e-106; Indels 0; Gaps 0;
Matches 121; Conservative 0; Mismatches 0;
Qy 1 MLGRAVMLLLPWTAGRAVPGSSPAWTCQQLSQKLTCLAWSAPLVGHMDLREEG 60
Db 1 MLGRAVMLLLPWTAGRAVPGSSPAWTCQQLSQKLTCLAWSAPLVGHMDLREEG 60
Qy 61 DEETNDVPHIQCGDGPQGLRDNSQFCLQRIHQGLIFYEKLIGSDIFTGEPSPLLPSP 120
Db 61 DEETNDVPHIQCGDGPQGLRDNSQFCLQRIHQGLIFYEKLIGSDIFTGEPSPLLPSP 120
Qy 121 V 121
Db 121 V 121

RESULT 5
Q2Q586 FELCA PRELIMINARY; PRT; 185 AA.
ID Q2Q586_FELCA
AC Q2Q586;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DT 07-FEB-2006, entry version 2.
DE Interleukin 23 p19 subunit (Fragment).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Felinae; Felis.
OX NCBI_TaxID=9685;
RN 1
RP NUCLEOTIDE SEQUENCE.
RA Peters I.R., Waly N.;
RL Submitted (SEP-2005) to the EMBL/GenBank/DBJ databases.
CC
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>

```
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; DQ195102; AB01676.1; -; mRNA.
FT NON TPR 185
SQ SEQUENCE 185 AA; 20433 MW; 344A2940A9PB773B CRC64;

Query Match 16.4%; Score 31; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 8.7e-21;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 DVPHIQGDCGDPGLRDNQFCLQRHQGL 97
Db 74 DVPHIQGDCGDPGLRDNQFCLQRHQGL 104

RESULT 6
Q9N2H9_PIG PRELIMINARY; PRT; 193 AA.
ID Q9N2H9_PIG
AC Q9N2H9;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE SGRF.
GN Name=SGRF; (Pig).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hirata Y., Kosuge Y.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AB030002; BAA93688.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR010831; IL23A.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR PANTHER; PTHR15947; IL23A; 1.
DR Pfam; PF00489; IL6; 1.
SQ SEQUENCE 193 AA; 21132 MW; 05F28DE94810B9E1 CRC64;

Query Match 13.2%; Score 25; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 4.7e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 164 KILRSLOAFVAAVFAHGAATLS 188
Db 168 KILRSLOAFVAAVFAHGAATLS 192

RESULT 7
Q64FUL_HORSE PRELIMINARY; PRT; 192 AA.
ID Q64FUL_HORSE
AC Q64FUL;
DT 25-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Interleukin 23 p19 subunit.
OS Equus caballus (Horse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Musilova P., Kubickova S., Vychodilova-Krenkova L., Kralik P.,
RX PubMed=16293125;
```

```
RA Matiasovic J., Hubertova D., Rubes J., Horin P.;
RT "Cytogenetic mapping of immunity-related genes in the domestic
RT horse.";
RL Anim. Genet. 36:507-510 (2005).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AV704416; AAU13947.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR010831; IL23A.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR PANTHER; PTHR15947; IL23A; 1.
DR Pfam; PF00489; IL6; 1.
SQ SEQUENCE 192 AA; 21042 MW; 9898C79BC9E22E4F CRC64;

Query Match 12.7%; Score 24; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 4.2e-14;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 164 KILRSLOAFVAAVFAHGAATL 187
Db 167 KILRSLOAFVAAVFAHGAATL 190

RESULT 8
Q6LA37_CAVPO PRELIMINARY; PRT; 189 AA.
ID Q6LA37_CAVPO
AC Q6LA37;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Interleukin-23 p19 subunit.
GN Name=IL-23 p19 subunit;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Shiratori I., Seya T.;
RL "Molecular cloning and functional characterization of guinea pig
RL Interleukin -23."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AB058509; BAD21123.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR010831; IL23A.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR PANTHER; PTHR15947; IL23A; 1.
DR Pfam; PF00489; IL6; 1.
SQ SEQUENCE 189 AA; 20808 MW; BE06A3C59955337F CRC64;

Query Match 10.6%; Score 20; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 WTQCQLSQKLCCTLAWSAHP 49
Db 30 WTQCQLSQKLCCTLAWSAHP 49
```



```
RESULT 9
Q91284 RAT
ID Q91284_RAT PRELIMINARY; PRT; 196 AA.
AC Q91284;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Interleukin 23, alpha subunit p19.
GN Name=IL23a;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=LEW;
RA Tran G., Hodgkinson S.;
RT "Rattus norvegicus IL-23 mRNA.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.L., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RG NIH MGC Project;
RG NIH MGC Project;
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
-----
DR EMBL; AY055379; AAL18223.1; -; mRNA.
DR EMBL; BC098907; AAH98907.1; -; mRNA.
DR Ensembl; ENSRNOG0000003254; Rattus norvegicus.
DR RGD; 620873; IL23a.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR010831; IL23A.
DR InterPro; IPR003573; IL6 MGF GCSP.
DR PANTHER; PTHR15947; IL23A; 1.
DR Pfam; PF00489; IL6; 1.
SQ SEQUENCE 196 AA; 21986 MW; 189F74BC409A961 CRC64;

Query Match 8.5%; Score 16; DB 2; Length 196;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

106 SDIFTEPSLLPDSVP 121
|||||
```

```
Db 107 SDIFTEPSLLPDSVP 122

RESULT 10
Q90WE2 PERMA
ID Q90WE2_PERMA PRELIMINARY; PRT; 184 AA.
AC Q90WE2;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Interleukin-23a subunit p19 (Fragment).
OS Peromyscus maniculatus (Deer mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Cricetidae; Neotominae; Peromyscus.
OX NCBI_TaxID=10042;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Schoutz T.;
RT "Cloning of deer mouse interleukin-23a p19 subunit.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
-----
DR EMBL; AY259629; AAP15041.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR010831; IL23A.
DR InterPro; IPR003573; IL6 MGF GCSP.
DR PANTHER; PTHR15947; IL23A; 1.
DR Pfam; PF00489; IL6; 1.
FT NON TER 184 184
SQ SEQUENCE 184 AA; 20850 MW; 4045456CF6ACA1C8 CRC64;

Query Match 7.4%; Score 14; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 DNSQFCLQRIHQGL 97
|||||
Db 84 DNSQFCLQRIHQGL 97

RESULT 11
Q9EQ14 MOUSE
ID Q9EQ14_MOUSE PRELIMINARY; PRT; 196 AA.
AC Q9EQ14;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Interleukin 23 p19 subunit (Interleukin 23, alpha subunit p19).
GN Name=IL23a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20567322; PubMed=11114383; DOI=10.1016/S1074-7613(00)00070-4;
RA Oppmann B., Lesley R., Blom B., Timans J.C., Xu Y., Hunte B., Vega F.,
RA Yu N., Wang J., Singh K., Zonin F., Vaisberg E., Churakova T.,
RA Liu M.-R., Gorman D., Wagner J., Zurawski S., Liu Y.-J., Abrams J.S.,
RA Moore K.W., Rennick D., de Waal-Malefyt R., Hannum C., Bazan J.F.,
RA Kastelein R.A.;
RT "Novel p19 protein engages IL-12p40 to form a cytokine, IL-23, with
RT biological activities similar as well as distinct from IL-12.";
RL Immunity 13:715-725(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
```

```
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RG NIH MGC Project;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF301619; AAG37231.1; -; mRNA.
DR EMBL; BC019953; ANH19953.1; -; mRNA.
DR Ensembl; ENSMUSG00000025383; Mus musculus.
DR MGI; MGI:1932410; IL23a.
DR GO; GO:0005615; C:extracellular space; RCA.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR010831; IL23A.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR PAM; PF00489; IL6; 1.
DR ProDom; PD004356; Interleukin_6; 1.
SQ SEQUENCE 196 AA; 22071 MW; DAF4A318A2DD3B7C CRC64;

Query Match 6.3%; Score 12; DB 2; Length 196;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 127 SLIGLSQLQPE 138
Db 128 SLIGLSQLQPE 139
|||||
127 SLIGLSQLQPE 138
128 SLIGLSQLQPE 139

RESULT 12
Q4V817_XENLA
ID Q4V817_XENLA PRELIMINARY; PRT; 151 AA.
AC Q4V817;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
[1]
RP NUCLEOTIDE SEQUENCE
RC TISSUE=Ovary;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
```

```
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovary;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BC097607; AAH97607.1; -; mRNA.
DR Hypothetical protein.
KW SSSEQUENCE 151 AA; 17574 MW; 4CAD3E036FF461B6 CRC64;

Query Match 4.8%; Score 9; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 AQGRAVPGG 25
Db 7 AQGRAVPGG 15
|||||
17 AQGRAVPGG 25
7 AQGRAVPGG 15

RESULT 13
Q4KJ01_PSEF5
ID Q4KJ01_PSEF5 PRELIMINARY; PRT; 538 AA.
AC Q4KJ01;
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Probable permease of ABC transporter PA4859.
GN OrderedLocustNames=PFL_0640;
OS Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=220664;
[1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15980861; DOI=10.1038/nbt1110;
RA Paulsen I.T., Press C.M., Ravel J., Kobayashi D.Y., Myers G.S.A.,
RA Mavrodi D.V., DeBoy R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J.,
RA Darkin A.S., Brinkac L.M., Daugherty S.C., Sullivan S.A.,
RA Rosovitz M.J., Gwinn M.L., Zhou L., Schneider D.J., Cartinhour S.W.,
RA Nelson W.C., Weidman J., Watkins K., Tran K., Khouri H., Pierson E.A.,
RA Pierson L.S. III, Thomashow L.S., Loper J.E.;
RT "Complete genome sequence of the plant commensal Pseudomonas
RT fluorescens Pf-5.";
```

```

RL Nat. Biotechnol. 23:873-878(2005).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CP000076; AAY96047.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; F:transport; IEA.
DR InterPro; IPR001851; Bac_inmem_transp.
DR Pfam; PF02653; BFD_transp_2; 1.
KW Complete proteome.
SQ SEQUENCE 538 AA; 56824 MW; 6976E2EB1BFA58D0 CRC64;

Query Match 4.2%; Score 9; DB 2; Length 538;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LLLLPWTAQ 18
Db 51 LLLLPWTAQ 59

RESULT 14
Q6IM10 DROME PRELIMINARY; PRT; 102 AA.
AC Q6IM10;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE HDC07858.
GN ORFNames=HDC07858;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed14709175; DOI=10.1186/gb-2003-5-1-r3;
RA Hild M., Beckmann B., Haas S.A., Koch B., Solovyev V., Busold C.,
RA Fellenberg K., Boutros M., Vingron M., Sauer F., Hoheisel J.D.,
RA Paro R.;
RT "An integrated gene annotation and transcriptional profiling approach
RT towards the full gene content of the Drosophila genome.";
RL Genome Biol. 5:RESEARCH0003.17(2003).
CC -!- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BK001856; DAA02702.1; -; Genomic DNA.
SQ SEQUENCE 102 AA; 10874 MW; 87EABD1E1318C175 CRC64;

Query Match 4.2%; Score 8; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 173 VAVAAARVF 180
Db 21 VAVAAARVF 28

RESULT 15
Q4S5N0 TETNG PRELIMINARY; PRT; 129 AA.
AC Q4S5N0;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Chromosome 9 SCAP14729, whole genome shotgun sequence. (Fragment).

```

```

GN ORFNames=GSTENG00023659001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraontoidea; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed15496914; DOI=10.1038/nature03025;
RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaut S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Bionnot C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutancieu J.-P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Keillis M., Wolff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CAAB01014729; CAG04052.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 129 AA; 13487 MW; 31DF806A16C687B5 CRC64;

Query Match 4.2%; Score 8; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 AVPGGSSP 28
Db 59 AVPGGSSP 66

Search completed: June 20, 2006, 04:58:47
Job time : 194.945 secs

```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2006, 04:59:09 ; Search time 35.8364 Seconds
(without alignments)
461.634 Million cell updates/sec

Title: US-10-797-157-2

Perfect score: 189

Sequence: 1 MLGSRVAMLLLLPWTAGR.....QAFVAARVFAHGAATLSP 189

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 650591 seqs, 87530628 residues

Word size : 1

Total number of hits satisfying chosen parameters: 649417

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /EMC_Celerra_IDS3/ptodata/2/iaa/5 COMB.pcp.*
- 2: /EMC_Celerra_IDS3/ptodata/2/iaa/6 COMB.pcp.*
- 3: /EMC_Celerra_IDS3/ptodata/2/iaa/7 COMB.pcp.*
- 4: /EMC_Celerra_IDS3/ptodata/2/iaa/H COMB.pcp.*
- 5: /EMC_Celerra_IDS3/ptodata/2/iaa/PCTUS COMB.pcp.*
- 6: /EMC_Celerra_IDS3/ptodata/2/iaa/RE COMB.pcp.*
- 7: /EMC_Celerra_IDS3/ptodata/2/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	189	100.0	189	2	US-09-122-443-2
2	189	100.0	189	2	US-09-558-089-2
3	189	100.0	189	2	US-09-558-087-2
4	189	100.0	189	2	US-09-558-474-2
5	189	100.0	189	6	US-09-935-366A-2
6	121	64.0	189	2	US-09-687-637B-1
7	54	28.6	54	2	US-09-687-637B-22
8	53	28.0	53	2	US-09-687-637B-25
9	34	18.0	49	2	US-09-687-637B-24
10	33	17.5	33	2	US-09-687-637B-23
11	25	13.2	102	2	US-09-122-443-5
12	25	13.2	102	2	US-09-558-089-5
13	25	13.2	102	2	US-09-558-087-5
14	25	13.2	102	2	US-09-558-474-5
15	25	13.2	102	6	US-09-935-366A-5
16	12	6.3	196	2	US-09-122-443-4
17	12	6.3	196	2	US-09-558-089-4
18	12	6.3	196	2	US-09-558-087-4
19	12	6.3	196	2	US-09-558-474-4
20	12	6.3	196	6	US-09-935-366A-4
21	8	4.2	232	2	US-09-252-991A-27938
22	8	4.2	282	2	US-09-248-756A-17514
23	8	4.2	542	2	US-09-252-991A-20276
24	7	3.7	21	2	US-08-481-968A-14
25	7	3.7	21	2	US-08-154-712B-14
26	7	3.7	21	2	US-09-947-925A-14

27	7	3.7	92	2	US-09-370-838-211	Sequence 211, Appl
28	7	3.7	92	2	US-09-854-133-211	Sequence 211, Appl
29	7	3.7	105	2	US-09-489-039A-9703	Sequence 9703, Ap
30	7	3.7	111	2	US-09-949-016-7690	Sequence 7690, Ap
31	7	3.7	117	1	US-08-505-617-6	Sequence 6, Appl
32	7	3.7	117	1	US-09-018-170-6	Sequence 6, Appl
33	7	3.7	146	2	US-09-270-767-33092	Sequence 33092, A
34	7	3.7	146	2	US-09-270-767-48309	Sequence 48309, A
35	7	3.7	155	2	US-09-975-456B-10	Sequence 10, Appl
36	7	3.7	165	2	US-08-966-317-1	Sequence 1, Appl
37	7	3.7	165	2	US-09-489-770-1	Sequence 1, Appl
38	7	3.7	178	2	US-09-252-991A-20936	Sequence 20936, A
39	7	3.7	178	2	US-09-252-991A-21443	Sequence 21443, A
40	7	3.7	181	2	US-09-605-703B-1344	Sequence 1344, Ap
41	7	3.7	189	2	US-09-332-934-13	Sequence 13, Appl
42	7	3.7	189	2	US-09-949-016-6103	Sequence 6103, Ap
43	7	3.7	202	2	US-08-256-847C-2	Sequence 2, Appl
44	7	3.7	206	2	US-10-094-749-2557	Sequence 2557, Ap
45	7	3.7	217	2	US-09-270-767-46068	Sequence 46068, A

ALIGNMENTS

RESULT 1
US-09-122-443-2
; Sequence 2, Application US/09122443
; Patent No. 6060284
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/122,443
; FILING DATE: 24-JUL-1998
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,765
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 189 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-122-443-2

Query Match 100.0%; Score 189; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 1.8e-167;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLGSRVAMLLLLPWTAGRVPCCSPAWTCCQOLSQKLCCTLAWSAHLVGHMDLREEG 60
Db 1 MLGSRVAMLLLLPWTAGRVPCCSPAWTCCQOLSQKLCCTLAWSAHLVGHMDLREEG 60

Qy 61 DEETTNDVPHIQCGDCDPOGLRDNSQFCLQRHQGLIFYEKLGSDFITGEPSSLDPSP 120
Db |||||
61 DEETTNDVPHIQCGDCDPOGLRDNSQFCLQRHQGLIFYEKLGSDFITGEPSSLDPSP 120
Qy 121 VAQLHASLLGLSQLOPEGHHWETQIQPSLSPSPQWQRLLRFLKILRSLOAFVAAARVF 180
Db |||||
121 VAQLHASLLGLSQLOPEGHHWETQIQPSLSPSPQWQRLLRFLKILRSLOAFVAAARVF 180
Qy 181 AHGAATLSP 189
Db |||||
181 AHGAATLSP 189
RESULT 2
US-09-558-089-2
; Sequence 2, Application US/09558089
; Patent No. 6479634
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/558,089
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/122,443
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 189 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-558-089-2
Query Match 100.0%; Score 189; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 1.8e-167;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLGSRVAMLLLLLPWTAQGRAVPGGSSPAWTCQQLSQKLTCLAWSAHPLVGHMDLREEG 60
Db 1 MLGSRVAMLLLLLPWTAQGRAVPGGSSPAWTCQQLSQKLTCLAWSAHPLVGHMDLREEG 60
Qy 61 DEETTNDVPHIQCGDCDPOGLRDNSQFCLQRHQGLIFYEKLGSDFITGEPSSLDPSP 120
Db |||||
61 DEETTNDVPHIQCGDCDPOGLRDNSQFCLQRHQGLIFYEKLGSDFITGEPSSLDPSP 120
Qy 121 VAQLHASLLGLSQLOPEGHHWETQIQPSLSPSPQWQRLLRFLKILRSLOAFVAAARVF 180
Db |||||
121 VAQLHASLLGLSQLOPEGHHWETQIQPSLSPSPQWQRLLRFLKILRSLOAFVAAARVF 180

Qy 181 AHGAATLSP 189
Db |||||
181 AHGAATLSP 189
RESULT 3
US-09-558-087-2
; Sequence 2, Application US/09558087
; Patent No. 6495667
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/558,087
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,765
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 189 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-558-087-2
Query Match 100.0%; Score 189; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 1.8e-167;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLGSRVAMLLLLLPWTAQGRAVPGGSSPAWTCQQLSQKLTCLAWSAHPLVGHMDLREEG 60
Db 1 MLGSRVAMLLLLLPWTAQGRAVPGGSSPAWTCQQLSQKLTCLAWSAHPLVGHMDLREEG 60
Qy 61 DEETTNDVPHIQCGDCDPOGLRDNSQFCLQRHQGLIFYEKLGSDFITGEPSSLDPSP 120
Db 61 DEETTNDVPHIQCGDCDPOGLRDNSQFCLQRHQGLIFYEKLGSDFITGEPSSLDPSP 120
Qy 121 VAQLHASLLGLSQLOPEGHHWETQIQPSLSPSPQWQRLLRFLKILRSLOAFVAAARVF 180
Db 121 VAQLHASLLGLSQLOPEGHHWETQIQPSLSPSPQWQRLLRFLKILRSLOAFVAAARVF 180
Qy 181 AHGAATLSP 189
Db |||||
181 AHGAATLSP 189
RESULT 4
US-09-558-474-2
; Sequence 2, Application US/09558474
; Patent No. 6835825

```

;
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 09/558,474
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,765
; FILING DATE: 25-JUL-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 189 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-558-474-2

Query Match 100.0%; Score 189; DB 2; Length 189;
Best Local Similarity 100.0%; Pred. No. 1.8e-167;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLGSAVMLLLPMTAQRAVPGSSPAWTCQQLSQKLCCTLAWSAHLVGHMDLREEG 60
Db 1 MLGSAVMLLLPMTAQRAVPGSSPAWTCQQLSQKLCCTLAWSAHLVGHMDLREEG 60

Qy 61 DEETTNDVPHIQCGDGPQGLRDNQSFCLQRIHQGLIFYEKLKLSQAFVAVARVF 120
Db 61 DEETTNDVPHIQCGDGPQGLRDNQSFCLQRIHQGLIFYEKLKLSQAFVAVARVF 120

Qy 121 VAQLHASLLGLSQLQPEGHWHWETQIIPSLSPSPQWQRLRLFKILRSIQAFVAVARVF 180
Db 121 VAQLHASLLGLSQLQPEGHWHWETQIIPSLSPSPQWQRLRLFKILRSIQAFVAVARVF 180

Qy 181 AHGAATLSP 189
Db 181 AHGAATLSP 189

RESULT 5
US-09-935-366A-2
; Sequence 2, Application US/09935366A
; Patent No. RE39015
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California

```

```

;
; COUNTRY: USA
; ZIP: 94304-1104
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/935,366A
; FILING DATE: 22-Aug-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/122,443
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 189 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-935-366A-2

Query Match 100.0%; Score 189; DB 6; Length 189;
Best Local Similarity 100.0%; Pred. No. 1.8e-167;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLGSAVMLLLPMTAQRAVPGSSPAWTCQQLSQKLCCTLAWSAHLVGHMDLREEG 60
Db 1 MLGSAVMLLLPMTAQRAVPGSSPAWTCQQLSQKLCCTLAWSAHLVGHMDLREEG 60

Qy 61 DEETTNDVPHIQCGDGPQGLRDNQSFCLQRIHQGLIFYEKLKLSQAFVAVARVF 120
Db 61 DEETTNDVPHIQCGDGPQGLRDNQSFCLQRIHQGLIFYEKLKLSQAFVAVARVF 120

Qy 121 VAQLHASLLGLSQLQPEGHWHWETQIIPSLSPSPQWQRLRLFKILRSIQAFVAVARVF 180
Db 121 VAQLHASLLGLSQLQPEGHWHWETQIIPSLSPSPQWQRLRLFKILRSIQAFVAVARVF 180

Qy 181 AHGAATLSP 189
Db 181 AHGAATLSP 189

RESULT 6
US-09-687-637B-1
; Sequence 1, Application US/09687637B
; Patent No. 6610285
; GENERAL INFORMATION:
; APPLICANT: Hirata, Yuichi
; TITLE OF INVENTION: CYTOKINE-LIKE PROTEINS THAT PROMOTE CELL PROLIFERATION
; FILE REFERENCE: 06501-067001
; CURRENT APPLICATION NUMBER: US/09/687,637B
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: PCT/JP99/01997
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: JP 10/121805
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-687-637B-1

```

Query Match 64.0%; Score 121; DB 2; Length 189;
 Best Local Similarity 100.0%; Pred. No. 2.2e-104;
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLGSRVALLLLPWTAGRAVPGSSPAWTCQQLSQKLTLSAHPVLVGHMDLREEG 60
 Db 1 MLGSRVALLLLPWTAGRAVPGSSPAWTCQQLSQKLTLSAHPVLVGHMDLREEG 60

Qy 61 DEETNDVPHIQCGDGPGLRDNQFCLORIHQGLIFYEKLGSDFITGEPSSLDPSP 120
 Db 61 DEETNDVPHIQCGDGPGLRDNQFCLORIHQGLIFYEKLGSDFITGEPSSLDPSP 120

Qy 121 V 121
 Db 121 V 121

RESULT 7
 US-09-687-637B-22
 ; Sequence 22, Application US/09687637B
 ; Patent No. 6610285
 ; GENERAL INFORMATION:
 ; APPLICANT: Hirata, Yuichi
 ; TITLE OF INVENTION: CYTOKINE-LIKE PROTEINS THAT PROMOTE CELL PROLIFERATION
 ; FILE REFERENCE: 06501-067001
 ; CURRENT APPLICATION NUMBER: US/09/687,637B
 ; CURRENT FILING DATE: 2000-10-13
 ; PRIOR APPLICATION NUMBER: PCT/JP99/01997
 ; PRIOR FILING DATE: 1999-04-14
 ; PRIOR APPLICATION NUMBER: JP 10/121805
 ; PRIOR FILING DATE: 1998-04-14
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 22
 ; LENGTH: 54
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-687-637B-22

Query Match 28.6%; Score 54; DB 2; Length 54;
 Best Local Similarity 100.0%; Pred. No. 1e-42;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLGSRVALLLLPWTAGRAVPGSSPAWTCQQLSQKLTLSAHPVLVGHM 54
 Db 1 MLGSRVALLLLPWTAGRAVPGSSPAWTCQQLSQKLTLSAHPVLVGHM 54

RESULT 8
 US-09-687-637B-25
 ; Sequence 25, Application US/09687637B
 ; Patent No. 6610285
 ; GENERAL INFORMATION:
 ; APPLICANT: Hirata, Yuichi
 ; TITLE OF INVENTION: CYTOKINE-LIKE PROTEINS THAT PROMOTE CELL PROLIFERATION
 ; FILE REFERENCE: 06501-067001
 ; CURRENT APPLICATION NUMBER: US/09/687,637B
 ; CURRENT FILING DATE: 2000-10-13
 ; PRIOR APPLICATION NUMBER: PCT/JP99/01997
 ; PRIOR FILING DATE: 1999-04-14
 ; PRIOR APPLICATION NUMBER: JP 10/121805
 ; PRIOR FILING DATE: 1998-04-14
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 25
 ; LENGTH: 53
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-687-637B-25

Query Match 28.0%; Score 53; DB 2; Length 53;
 Best Local Similarity 100.0%; Pred. No. 8.6e-42;
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 137 PEGHWETQOIPSLSPQWRLLRFLKILRSIQAFVAVARVFAHGAATLSP 189
 Db 1 PEGHWETQOIPSLSPQWRLLRFLKILRSIQAFVAVARVFAHGAATLSP 53

RESULT 9
 US-09-687-637B-24
 ; Sequence 24, Application US/09687637B
 ; Patent No. 6610285
 ; GENERAL INFORMATION:
 ; APPLICANT: Hirata, Yuichi
 ; TITLE OF INVENTION: CYTOKINE-LIKE PROTEINS THAT PROMOTE CELL PROLIFERATION
 ; FILE REFERENCE: 06501-067001
 ; CURRENT APPLICATION NUMBER: US/09/687,637B
 ; CURRENT FILING DATE: 2000-10-13
 ; PRIOR APPLICATION NUMBER: PCT/JP99/01997
 ; PRIOR FILING DATE: 1999-04-14
 ; PRIOR APPLICATION NUMBER: JP 10/121805
 ; PRIOR FILING DATE: 1998-04-14
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 24
 ; LENGTH: 49
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-687-637B-24

Query Match 18.0%; Score 34; DB 2; Length 49;
 Best Local Similarity 100.0%; Pred. No. 3.4e-24;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 88 FCLQRIHQGLIFYEKLGSDFITGEPSSLDPSPV 121
 Db 1 FCLQRIHQGLIFYEKLGSDFITGEPSSLDPSPV 34

RESULT 10
 US-09-687-637B-23
 ; Sequence 23, Application US/09687637B
 ; Patent No. 6610285
 ; GENERAL INFORMATION:
 ; APPLICANT: Hirata, Yuichi
 ; TITLE OF INVENTION: CYTOKINE-LIKE PROTEINS THAT PROMOTE CELL PROLIFERATION
 ; FILE REFERENCE: 06501-067001
 ; CURRENT APPLICATION NUMBER: US/09/687,637B
 ; CURRENT FILING DATE: 2000-10-13
 ; PRIOR APPLICATION NUMBER: PCT/JP99/01997
 ; PRIOR FILING DATE: 1999-04-14
 ; PRIOR APPLICATION NUMBER: JP 10/121805
 ; PRIOR FILING DATE: 1998-04-14
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 23
 ; LENGTH: 33
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-687-637B-23

Query Match 17.5%; Score 33; DB 2; Length 33;
 Best Local Similarity 100.0%; Pred. No. 2e-23;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 DLREEGDEETNDVPHIQCGDGPGLRDNQ 87
 Db 1 DLREEGDEETNDVPHIQCGDGPGLRDNQ 33

RESULT 11
 US-09-122-443-5
 ; Sequence 5, Application US/09122443
 ; Patent No. 6060284
 ; GENERAL INFORMATION:


```

;
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-558-089-5

Query Match 13.2%; Score 25; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0

QY 164 KILRSIQAFVAVAAARVFAHGAATLS 188
DB 77 KILRSIQAFVAVAAARVFAHGAATLS 101

RESULT 13
US-09-558-087-5
; Sequence 5, Application US/09558087
; Patent No. 6495667
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/558,087
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,765
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-558-087-5

Query Match 13.2%; Score 25; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.5e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0

```

CLTY: Palo Alto
STATE: California

Search completed: June 20, 2006, 05:01:01
Job time : 36.8364 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2006, 04:59:59 ; Search time 132.055 Seconds
(without alignments)
662.966 Million cell updates/sec

Title: US-10-797-157-2

Perfect score: 189

Sequence: 1 MLGSRVNMILLLEPWTQAGR.....QAFVAVAAARVFAHGAATLSP 189

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2097797 seqs, 463214858 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2096646

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	189	100.0	189	4	US-10-375-706-2
2	189	100.0	189	4	US-10-742-405-4
3	189	100.0	189	5	US-10-797-157-2
4	189	100.0	189	5	US-10-720-026-6
5	189	100.0	189	6	US-11-006-154-2
6	170	89.9	521	4	US-10-742-405-8
7	170	89.9	521	5	US-10-797-157-11
8	121	64.0	189	3	US-09-965-528-14
9	121	64.0	189	3	US-09-374-046A-138
10	121	64.0	189	3	US-09-969-984-14
11	121	64.0	189	4	US-10-028-072-232
12	121	64.0	189	4	US-10-140-808-232
13	121	64.0	189	4	US-10-121-049-232
14	121	64.0	189	4	US-10-123-904-232
15	121	64.0	189	4	US-10-140-470-232
16	121	64.0	189	4	US-10-175-746-232
17	121	64.0	189	4	US-10-176-918-232
18	121	64.0	189	4	US-10-176-921-232
19	121	64.0	189	4	US-10-137-865-232
20	121	64.0	189	4	US-10-140-474-232
21	121	64.0	189	4	US-10-142-431-232
22	121	64.0	189	4	US-10-143-114-232
23	121	64.0	189	4	US-10-142-419-232
24	121	64.0	189	4	US-10-123-262-232
25	121	64.0	189	4	US-10-142-423-232
26	121	64.0	189	4	US-10-121-050-232
27	121	64.0	189	4	US-10-141-755-232

28	121	64.0	189	4	US-10-143-032-232	Sequence 232, App
29	121	64.0	189	4	US-10-123-108-232	Sequence 232, App
30	121	64.0	189	4	US-10-123-236-232	Sequence 232, App
31	121	64.0	189	4	US-10-123-261-232	Sequence 232, App
32	121	64.0	189	4	US-10-140-921-232	Sequence 232, App
33	121	64.0	189	4	US-10-140-928-232	Sequence 232, App
34	121	64.0	189	4	US-10-121-045-232	Sequence 232, App
35	121	64.0	189	4	US-10-123-292-232	Sequence 232, App
36	121	64.0	189	4	US-10-123-903-232	Sequence 232, App
37	121	64.0	189	4	US-10-124-819-232	Sequence 232, App
38	121	64.0	189	4	US-10-124-822-232	Sequence 232, App
39	121	64.0	189	4	US-10-140-925-232	Sequence 232, App
40	121	64.0	189	4	US-10-160-498-232	Sequence 232, App
41	121	64.0	189	4	US-10-124-824-232	Sequence 232, App
42	121	64.0	189	4	US-10-127-825A-232	Sequence 232, App
43	121	64.0	189	4	US-10-127-829A-232	Sequence 232, App
44	121	64.0	189	4	US-10-127-835A-232	Sequence 232, App
45	121	64.0	189	4	US-10-127-839A-232	Sequence 232, App

ALIGNMENTS

RESULT 1
US-10-375-706-2
; Sequence 2, Application US/10375706
; Publication No. US20030162261A1
; GENERAL INFORMATION:
; APPLICANT: De Waal Malefyt, Rene
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Lira, Sergio A.
; APPLICANT: Narula, Satwant
; APPLICANT: Oppmann, Birgit
; APPLICANT: Rennick, Donna M.
; APPLICANT: Wikowski, Maria
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
; FILE REFERENCE: DX01042X US
; CURRENT APPLICATION NUMBER: US/10/375,706
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US/09/658,699
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 09/393,090
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 60/164,616
; PRIOR FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: surmised Homo sapiens
US-10-375-706-2

Query Match	100.0%	Score 189;	DB 4;	Length 189;
Best Local Similarity	100.0%;	Pred. No. 3.8e-163;	Mismatches 0;	Indels 0;
Matches 189;	Conservative	0;		Gaps 0;
QY	1	MLGSRVNMILLLEPWTQAGR	VPGSSPAWTCQOOLSQKCLCTLAWSAHLVGHMDLREEG	60
Db	1	MLGSRVNMILLLEPWTQAGR	VPGSSPAWTCQOOLSQKCLCTLAWSAHLVGHMDLREEG	60
QY	61	DEETNDVPHTQCGDGDPOGLRDN	SPQCLQRIHQGLIFYEKLIGSDIFTGPSP	120
Db	61	DEETNDVPHTQCGDGDPOGLRDN	SPQCLQRIHQGLIFYEKLIGSDIFTGPSP	120
QY	121	VAQHASLILGHSQLOPEGHWHW	QQIPSLSPSQPWORLLRFRKILRSIQAFVAAVAVF	180
Db	121	VAQHASLILGHSQLOPEGHWHW	QQIPSLSPSQPWORLLRFRKILRSIQAFVAAVAVF	180
QY	181	AHGAATLSP	189	

```
Db      181 AHGAATLSP 189
|||||||
RESULT 2
US-10-742-405-4
; Sequence 4, Application US/10742405
; Publication No. US20040213761A1
; GENERAL INFORMATION:
; APPLICANT: Bowman, Edward P.
; APPLICANT: Chan, Jason R.
; APPLICANT: Moore, Kevin
; APPLICANT: Nguyen, Nhung
; APPLICANT: Churakova, Tatyana
; APPLICANT: Chen, Shi-Juan
; APPLICANT: Cua, Daniel J.
; TITLE OF INVENTION: Uses of mammalian cytokine; related reagents
; FILE REFERENCE: DX01578K
; CURRENT APPLICATION NUMBER: US/10/742,405
; NUMBER FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-742-405-4
Query Match      100.0%; Score 189; DB 4; Length 189;
Best Local Similarity 100.0%; Pred. No. 3.8e-163;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 MLGSRVAMLLLLLPWTAQGRAVPGSSPAWTCQOOLSQKLTLSAWSAHPLVGHMDLREEG 60
Db      1 MLGSRVAMLLLLLPWTAQGRAVPGSSPAWTCQOOLSQKLTLSAWSAHPLVGHMDLREEG 60
|
Qy      61 DEETTNDVPHIQCGDGDPCQGLRDNQFCQLRIHQGLIFYEKLIGSDIFTGEPSSLDPSP 120
Db      61 DEETTNDVPHIQCGDGDPCQGLRDNQFCQLRIHQGLIFYEKLIGSDIFTGEPSSLDPSP 120
|
Qy      121 VAQHASLLGLSLLQLOPEGHHWETQIIPSLSPSPQWQRLRLRPFKILRSLOAFVAAARVF 180
Db      121 VAQHASLLGLSLLQLOPEGHHWETQIIPSLSPSPQWQRLRLRPFKILRSLOAFVAAARVF 180
|
Qy      181 AHGAATLSP 189
Db      181 AHGAATLSP 189
|
RESULT 4
US-10-720-026-6
; Sequence 6, Application US/10720026
; Publication No. US20040258686A1
; GENERAL INFORMATION:
; APPLICANT: Chirica, Madaline
; APPLICANT: Parham, Christi L.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Moore, Kevin W.
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.
; FILE REFERENCE: DX01074BiK
; CURRENT APPLICATION NUMBER: US/10/720,026
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: 60/203,426
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-720-026-6
Query Match      100.0%; Score 189; DB 5; Length 189;
Best Local Similarity 100.0%; Pred. No. 3.8e-163;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 MLGSRVAMLLLLLPWTAQGRAVPGSSPAWTCQOOLSQKLTLSAWSAHPLVGHMDLREEG 60
Db      1 MLGSRVAMLLLLLPWTAQGRAVPGSSPAWTCQOOLSQKLTLSAWSAHPLVGHMDLREEG 60
|
Qy      61 DEETTNDVPHIQCGDGDPCQGLRDNQFCQLRIHQGLIFYEKLIGSDIFTGEPSSLDPSP 120
Db      61 DEETTNDVPHIQCGDGDPCQGLRDNQFCQLRIHQGLIFYEKLIGSDIFTGEPSSLDPSP 120
|
Qy      121 VAQHASLLGLSLLQLOPEGHHWETQIIPSLSPSPQWQRLRLRPFKILRSLOAFVAAARVF 180
Db      121 VAQHASLLGLSLLQLOPEGHHWETQIIPSLSPSPQWQRLRLRPFKILRSLOAFVAAARVF 180
|
Qy      181 AHGAATLSP 189
Db      181 AHGAATLSP 189
|
RESULT 5
US-11-006-154-2
; Sequence 2, Application US/11006154
; Publication No. US20050158750A1
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
;
Qy      1 MLGSRVAMLLLLLPWTAQGRAVPGSSPAWTCQOOLSQKLTLSAWSAHPLVGHMDLREEG 60
Db      1 MLGSRVAMLLLLLPWTAQGRAVPGSSPAWTCQOOLSQKLTLSAWSAHPLVGHMDLREEG 60
|
Qy      61 DEETTNDVPHIQCGDGDPCQGLRDNQFCQLRIHQGLIFYEKLIGSDIFTGEPSSLDPSP 120
Db      61 DEETTNDVPHIQCGDGDPCQGLRDNQFCQLRIHQGLIFYEKLIGSDIFTGEPSSLDPSP 120
|
Qy      121 VAQHASLLGLSLLQLOPEGHHWETQIIPSLSPSPQWQRLRLRPFKILRSLOAFVAAARVF 180
Db      121 VAQHASLLGLSLLQLOPEGHHWETQIIPSLSPSPQWQRLRLRPFKILRSLOAFVAAARVF 180
|
Qy      181 AHGAATLSP 189
Db      181 AHGAATLSP 189
|
Query Match      100.0%; Score 189; DB 5; Length 189;
Best Local Similarity 100.0%; Pred. No. 3.8e-163;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 MLGSRVAMLLLLLPWTAQGRAVPGSSPAWTCQOOLSQKLTLSAWSAHPLVGHMDLREEG 60
Db      1 MLGSRVAMLLLLLPWTAQGRAVPGSSPAWTCQOOLSQKLTLSAWSAHPLVGHMDLREEG 60
|
Qy      61 DEETTNDVPHIQCGDGDPCQGLRDNQFCQLRIHQGLIFYEKLIGSDIFTGEPSSLDPSP 120
Db      61 DEETTNDVPHIQCGDGDPCQGLRDNQFCQLRIHQGLIFYEKLIGSDIFTGEPSSLDPSP 120
|
Qy      121 VAQHASLLGLSLLQLOPEGHHWETQIIPSLSPSPQWQRLRLRPFKILRSLOAFVAAARVF 180
Db      121 VAQHASLLGLSLLQLOPEGHHWETQIIPSLSPSPQWQRLRLRPFKILRSLOAFVAAARVF 180
|
Qy      181 AHGAATLSP 189
Db      181 AHGAATLSP 189
|
RESULT 3
US-10-797-157-2
; Sequence 2, Application US/10797157
; Publication No. US20040223969A1
; GENERAL INFORMATION:
; APPLICANT: Ofc, Martin
; APPLICANT: McClanahan, Terrill K.
; TITLE OF INVENTION: USES OF IL-23 AGONISTS AND ANTAGONISTS; RELATED REAGENTS
; FILE REFERENCE: DX06022US01
; CURRENT APPLICATION NUMBER: US/10/797,157
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: U.S. 60/453,672
; PRIOR FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-797-157-2
Query Match      100.0%; Score 189; DB 5; Length 189;
Best Local Similarity 100.0%; Pred. No. 3.8e-163;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/006,154
; FILING DATE: 06-Dec-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/935,366
; FILING DATE: 22-Aug-2001
; APPLICATION NUMBER: 09/122,443
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 189 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-11-006-154-2

Query Match 100.0%; Score 189; DB 6; Length 189;
Best Local Similarity 100.0%; Pred. No. 3.8e-163;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCGRAVMLLLPWTAGRAVPGSSPAWTCQQLSOKLCTLAWSAHPVGHMDLREEG 60
Db 1 MCGRAVMLLLPWTAGRAVPGSSPAWTCQQLSOKLCTLAWSAHPVGHMDLREEG 60

Qy 61 DEETNDVPHIQCGDPCQGLRNSQFCLORIHQGLIFYEKLGLSDIFTGEPSSLDPSP 120
Db 61 DEETNDVPHIQCGDPCQGLRNSQFCLORIHQGLIFYEKLGLSDIFTGEPSSLDPSP 120

Qy 121 VAQLHASLLGLSOLLQPEGHWHWETQIIPSLSPSQWQLRLFRKILRSLOAFVAVARVF 180
Db 121 VAQLHASLLGLSOLLQPEGHWHWETQIIPSLSPSQWQLRLFRKILRSLOAFVAVARVF 180

Qy 181 AHGAATLSP 189
Db 181 AHGAATLSP 189

RESULT 6
US-10-742-405-8
; Sequence 8, Application US/10742405
; Publication No. US20040213761A1
; GENERAL INFORMATION:
; APPLICANT: Bowman, Edward P.
; APPLICANT: Chan, Jason R.
; APPLICANT: Moore, Kevin
; APPLICANT: Nguyen, Nhung
; APPLICANT: Churakova, Tatyana
; APPLICANT: Chen, Shi-Juan
; APPLICANT: Cua, Daniel J.
; TITLE OF INVENTION: Uses of mammalian cytokine; related reagents
; FILE REFERENCE: DX01578K
; CURRENT APPLICATION NUMBER: US/10/742,405
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in version 3.2

; SEQ ID NO 8
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-742-405-8

Query Match 89.9%; Score 170; DB 4; Length 521;
Best Local Similarity 100.0%; Pred. No. 1.7e-145;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 RAVEGSSPAWTCQQLSOKLCTLAWSAHPVGHMDLREEGDEETNDVPHIQCGDGP 79
Db 352 RAVEGSSPAWTCQQLSOKLCTLAWSAHPVGHMDLREEGDEETNDVPHIQCGDGP 411

Qy 80 QGLRDSQFCLORIHQGLIFYEKLGLSDIFTGEPSSLDPSPVAQLHASLLGLSOLLQPEG 139
Db 412 QGLRDSQFCLORIHQGLIFYEKLGLSDIFTGEPSSLDPSPVAQLHASLLGLSOLLQPEG 471

Qy 140 HHWETQIIPSLSPSQWQLRLFRKILRSLOAFVAVARVFAHGAATLSP 189
Db 472 HHWETQIIPSLSPSQWQLRLFRKILRSLOAFVAVARVFAHGAATLSP 521

RESULT 7
US-10-797-157-11
; Sequence 11, Application US/10797157
; Publication No. US20040223969A1
; GENERAL INFORMATION:
; APPLICANT: Oft, Martin
; APPLICANT: McClanahan, Terrill K.
; TITLE OF INVENTION: USES OF IL-23 AGONISTS AND ANTAGONISTS; RELATED REAGENTS
; FILE REFERENCE: DX06022US01
; CURRENT APPLICATION NUMBER: US/10/797,157
; CURRENT FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: U.S. 60/453,672
; PRIOR FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 11
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-797-157-11

Query Match 89.9%; Score 170; DB 5; Length 521;
Best Local Similarity 100.0%; Pred. No. 1.7e-145;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 RAVEGSSPAWTCQQLSOKLCTLAWSAHPVGHMDLREEGDEETNDVPHIQCGDGP 79
Db 352 RAVEGSSPAWTCQQLSOKLCTLAWSAHPVGHMDLREEGDEETNDVPHIQCGDGP 411

Qy 80 QGLRDSQFCLORIHQGLIFYEKLGLSDIFTGEPSSLDPSPVAQLHASLLGLSOLLQPEG 139
Db 412 QGLRDSQFCLORIHQGLIFYEKLGLSDIFTGEPSSLDPSPVAQLHASLLGLSOLLQPEG 471

Qy 140 HHWETQIIPSLSPSQWQLRLFRKILRSLOAFVAVARVFAHGAATLSP 189
Db 472 HHWETQIIPSLSPSQWQLRLFRKILRSLOAFVAVARVFAHGAATLSP 521

RESULT 8
US-09-965-528-14
; Sequence 14, Application US/09965528
; Publication No. US20020187523A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: TANG, Y. Tom
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: BURFORD, Neil
; APPLICANT: BANDMAN, Olga
; APPLICANT: BAUGHN, Mariah R.

```

```
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: EXTRACELLULAR SIGNALING MOLECULES
; FILE REFERENCE: PF-0701 USA
; CURRENT APPLICATION NUMBER: US/09/965,528
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/134,949
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/144,270
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: 60/146,700
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/157,508
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PERL Program
; SEQ ID NO 14
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020187523A1 2933038CD1
; US-09-965-528-14

Query Match      64.0%; Score 121; DB 3; Length 189;
Best Local Similarity 100.0%; Pred. No. 2e-101;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MLGSRVAMLLLLLPWTAQGRAVPGSSPAWTCQQLSQKLTLSAWSAHPLVGHMDLREEG 60
Db      1  MLGSRVAMLLLLLPWTAQGRAVPGSSPAWTCQQLSQKLTLSAWSAHPLVGHMDLREEG 60

Qy      61 DEETTNDVPHIQCGDGDPOGLRDNQSFCLQRHQGLIFYEKLGSDFITGEPSLLPDSP 120
Db      61 DEETTNDVPHIQCGDGDPOGLRDNQSFCLQRHQGLIFYEKLGSDFITGEPSLLPDSP 120

Qy      121 V 121
Db      121 V 121

RESULT 9
US-09-374-046A-138
; Sequence 138, Application US/09374046A
; Publication No. US20030096951A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steinger II, Robert J.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fachtel, Kim
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6075-83A
; CURRENT APPLICATION NUMBER: US/09/374,046A
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 138
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-374-046A-138

Query Match      64.0%; Score 121; DB 3; Length 189;
Best Local Similarity 100.0%; Pred. No. 2e-101;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MLGSRVAMLLLLLPWTAQGRAVPGSSPAWTCQQLSQKLTLSAWSAHPLVGHMDLREEG 60
Db      1  MLGSRVAMLLLLLPWTAQGRAVPGSSPAWTCQQLSQKLTLSAWSAHPLVGHMDLREEG 60

Qy      61 DEETTNDVPHIQCGDGDPOGLRDNQSFCLQRHQGLIFYEKLGSDFITGEPSLLPDSP 120
Db      61 DEETTNDVPHIQCGDGDPOGLRDNQSFCLQRHQGLIFYEKLGSDFITGEPSLLPDSP 120

Qy      121 V 121
Db      121 V 121

RESULT 9
US-09-374-046A-138
; Sequence 138, Application US/09374046A
; Publication No. US20030096951A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steinger II, Robert J.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fachtel, Kim
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6075-83A
; CURRENT APPLICATION NUMBER: US/09/374,046A
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 138
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-374-046A-138
```

```
Query Match      64.0%; Score 121; DB 3; Length 189;
Best Local Similarity 100.0%; Pred. No. 2e-101;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MLGSRVAMLLLLLPWTAQGRAVPGSSPAWTCQQLSQKLTLSAWSAHPLVGHMDLREEG 60
Db      1  MLGSRVAMLLLLLPWTAQGRAVPGSSPAWTCQQLSQKLTLSAWSAHPLVGHMDLREEG 60

Qy      61 DEETTNDVPHIQCGDGDPOGLRDNQSFCLQRHQGLIFYEKLGSDFITGEPSLLPDSP 120
Db      61 DEETTNDVPHIQCGDGDPOGLRDNQSFCLQRHQGLIFYEKLGSDFITGEPSLLPDSP 120

Qy      121 V 121
Db      121 V 121

RESULT 10
US-09-969-984-14
; Sequence 14, Application US/09969984
; Publication No. US20040048244A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: TANG, Y. Tom
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: BURFORD, Neil
; APPLICANT: BANDMAN, Olga
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: EXTRACELLULAR SIGNALING MOLECULES
; FILE REFERENCE: PF-0701-1 USA
; CURRENT APPLICATION NUMBER: US/09/969,984
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/134,949; 60/144,270; 60/146,700; 60/157,508
; PRIOR FILING DATE: 1999-05-19; 1999-07-15; 1999-07-30; 1999-10-04
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PERL Program
; SEQ ID NO 14
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040048244A1 2933038CD1
; US-09-969-984-14

Query Match      64.0%; Score 121; DB 3; Length 189;
Best Local Similarity 100.0%; Pred. No. 2e-101;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MLGSRVAMLLLLLPWTAQGRAVPGSSPAWTCQQLSQKLTLSAWSAHPLVGHMDLREEG 60
Db      1  MLGSRVAMLLLLLPWTAQGRAVPGSSPAWTCQQLSQKLTLSAWSAHPLVGHMDLREEG 60

Qy      61 DEETTNDVPHIQCGDGDPOGLRDNQSFCLQRHQGLIFYEKLGSDFITGEPSLLPDSP 120
Db      61 DEETTNDVPHIQCGDGDPOGLRDNQSFCLQRHQGLIFYEKLGSDFITGEPSLLPDSP 120

Qy      121 V 121
Db      121 V 121

RESULT 11
US-10-028-072-232
; Sequence 232, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
```

APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Deenoys, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059836
PRIOR FILING DATE: 1997-09-24
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062285
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062814
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/062816
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063045
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063082
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/063127
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063327
PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063329
PRIOR FILING DATE: 1997-10-27
PRIOR APPLICATION NUMBER: 60/063550
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063561
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063704
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063733
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063735
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063738
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063755
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064248
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/064809
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065846
PRIOR FILING DATE: 1997-11-17
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066453
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066511
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/069212
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069278
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069334
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069694
PRIOR FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: 60/072320
PRIOR FILING DATE: 1998-01-23
PRIOR APPLICATION NUMBER: 60/073612
PRIOR FILING DATE: 1998-02-04
PRIOR APPLICATION NUMBER: 60/074086
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/074092
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-02-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081695
PRIOR FILING DATE: 1998-04-14
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081818
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082999
PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085149
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13

1	PRIOR APPLICATION NUMBER: 60/085338	
2	PRIOR FILING DATE: 1998-05-13	
3	PRIOR APPLICATION NUMBER: 60/085339	
4	PRIOR FILING DATE: 1998-05-13	
5	PRIOR APPLICATION NUMBER: 60/085579	
6	PRIOR FILING DATE: 1998-05-15	
7	PRIOR APPLICATION NUMBER: 60/085697	
8	PRIOR FILING DATE: 1998-05-15	
9	PRIOR APPLICATION NUMBER: 60/085704	
10	PRIOR FILING DATE: 1998-05-15	
11	PRIOR APPLICATION NUMBER: 60/086414	
12	PRIOR FILING DATE: 1998-05-22	
13	PRIOR APPLICATION NUMBER: 60/086430	
14	PRIOR FILING DATE: 1998-05-22	
15	PRIOR APPLICATION NUMBER: 60/087106	
16	PRIOR FILING DATE: 1998-05-28	
17	PRIOR APPLICATION NUMBER: 60/088026	
18	PRIOR FILING DATE: 1998-06-04	
19	PRIOR APPLICATION NUMBER: 60/088730	
20	PRIOR FILING DATE: 1998-06-10	
21	PRIOR APPLICATION NUMBER: 60/088741	
22	PRIOR FILING DATE: 1998-06-10	
23	PRIOR APPLICATION NUMBER: 60/088810	
24	PRIOR FILING DATE: 1998-06-10	
25	PRIOR APPLICATION NUMBER: 60/088858	
26	PRIOR FILING DATE: 19/98-06-11	
27	PRIOR APPLICATION NUMBER: 60/089532	
28	PRIOR FILING DATE: 1998-06-17	
29	PRIOR APPLICATION NUMBER: 60/089599	
30	PRIOR FILING DATE: 1998-06-17	
31	PRIOR APPLICATION NUMBER: 60/089907	
32	PRIOR FILING DATE: 1998-06-18	
33	PRIOR APPLICATION NUMBER: 60/089947	
34	PRIOR FILING DATE: 1998-06-19	
35	PRIOR APPLICATION NUMBER: 60/090349	
36	PRIOR FILING DATE: 1998-06-23	
37	PRIOR APPLICATION NUMBER: 60/090429	
38	PRIOR FILING DATE: 1998-06-24	
39	PRIOR APPLICATION NUMBER: 60/090445	
40	PRIOR FILING DATE: 1998-06-24	
41	PRIOR APPLICATION NUMBER: 60/090538	
42	PRIOR FILING DATE: 1998-06-24	
43	PRIOR APPLICATION NUMBER: 60/090863	
44	PRIOR FILING DATE: 1998-06-26	
45	PRIOR APPLICATION NUMBER: 60/091360	
46	PRIOR FILING DATE: 1998-07-01	
47	PRIOR APPLICATION NUMBER: 60/091519	
48	PRIOR FILING DATE: 1998-07-02	
49	PRIOR APPLICATION NUMBER: 60/091982	
50	PRIOR FILING DATE: 1998-07-07	

Query Match	64.0%;	Score 121;	DB 4;	Length 189;
Best Local Similarity	100.0%;	Pred. No. 2e-101;		
Matches 121;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MLGSRAVMLLLLLPWTAGRAVPGGSSPAWTCQOOLSQKLCCTLAWSAHPVGHMDLREEG	60	
Db	1	MLGSRAVMLLLLLPWTAGRAVPGGSSPAWTCQOOLSQKLCCTLAWSAHPVGHMDLREEG	60	
Qy	61	DEETTNDVPHIQCGDGCDDPGLRDNQSFCLQRIHQGLIFYEKLLGSDIFTGEPSSLDPSP	120	
Db	61	DEETTNDVPHIQCGDGCDDPGLRDNQSFCLQRIHQGLIFYEKLLGSDIFTGEPSSLDPSP	120	
Qy	121	V 121		
Db	121	V 121		

RESULT 12
US-10-140-808-232
; Sequence 232, Application US/10140808
; Publication No. US20030017563A1
; GENERAL INFORMATION:
; CURRENT APPLICATION NUMBER: US/10/121,049
; FILE REFERENCE: P3330R1C17
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; APPLICANT: Zhang, Zemin
; INVENTOR: Zhang, Zemin

```

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3310R1C182
; CURRENT APPLICATION NUMBER: US/10/140,808
; PRIORITY FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 232
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-140-808-232

Query Match 64.0%; Score 121; DB 4; Length 189;
Best Local Similarity 100.0%; Pred. No. 2e-101;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLCGRVAMLLLLLPWTAQGRAVPGSGSSPAWTCQQQLSOKLCTLAWSAHPVGHMDIREEG 60
Db 1 MLCGRVAMLLLLLPWTAQGRAVPGSGSSPAWTCQQQLSOKLCTLAWSAHPVGHMDIREEG 60

Qy 61 DEETTDNDVPHIQCGDGDPCQGLRDNSQFCQLRIHQGLIFVEKLLGSDIFTGEPSSLDPSP 120
Db 61 DEETTDNDVPHIQCGDGDPCQGLRDNSQFCQLRIHQGLIFVEKLLGSDIFTGEPSSLDPSP 120

Qy 121 V 121
Db 121 V 121

RESULT 13
US-10-121-049-232
; Sequence 232, Application US/10121049
; Publication No. US20030022239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3310R1C17
; CURRENT APPLICATION NUMBER: US/10/121,049

```

```

RESULT 13
US/10-121-049-232
; Sequence 23, Application US/10121049
; Publication No. US2003002239A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeGeorge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvarcoff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
;
; TITLE OF INVENTION: SECRETED AND TRA
;
; TITLE OF INVENTION: ACIDS ENCODING
;
; FILE REFERENCE: P3330R1C17
;
; CURRENT APPLICATION NUMBER: US/10/12

```


;
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 232
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-049-232

Query Match 64.0%; Score 121; DB 4; Length 189;
Best Local Similarity 100.0%; Pred. No. 2e-101;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSRAVMLLLPNTAAGRAVPGSSPAWTCQQLSOKLCTLAWSAHLVGHMDLREEG 60
DB 1 MGSRAVMLLLPNTAAGRAVPGSSPAWTCQQLSOKLCTLAWSAHLVGHMDLREEG 60

QY 61 DEETNDVPHIQCGDCDPQGLRDNQSQCFLQRIHQGLIFYEKLGSIDFTGEPSSLDPSP 120
DB 61 DEETNDVPHIQCGDCDPQGLRDNQSQCFLQRIHQGLIFYEKLGSIDFTGEPSSLDPSP 120

QY 121 V 121
DB 121 V 121

RESULT 14
US-10-123-904-232
; Sequence 232, Application US/10123904
; Publication No. US20030022328A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C54
; CURRENT APPLICATION NUMBER: US/10/123,904
; CURRENT FILING DATE: 2002-04-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 232
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-904-232

Query Match 64.0%; Score 121; DB 4; Length 189;
Best Local Similarity 100.0%; Pred. No. 2e-101;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSRAVMLLLPNTAAGRAVPGSSPAWTCQQLSOKLCTLAWSAHLVGHMDLREEG 60
DB 1 MGSRAVMLLLPNTAAGRAVPGSSPAWTCQQLSOKLCTLAWSAHLVGHMDLREEG 60

QY 61 DEETNDVPHIQCGDCDPQGLRDNQSQCFLQRIHQGLIFYEKLGSIDFTGEPSSLDPSP 120
DB 61 DEETNDVPHIQCGDCDPQGLRDNQSQCFLQRIHQGLIFYEKLGSIDFTGEPSSLDPSP 120

QY 121 V 121
DB 121 V 121

RESULT 15
US-10-140-470-232
; Sequence 232, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C160
; CURRENT APPLICATION NUMBER: US/10/140,470
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 232
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-470-232

Query Match 64.0%; Score 121; DB 4; Length 189;
Best Local Similarity 100.0%; Pred. No. 2e-101;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSRAVMLLLPNTAAGRAVPGSSPAWTCQQLSOKLCTLAWSAHLVGHMDLREEG 60
DB 1 MGSRAVMLLLPNTAAGRAVPGSSPAWTCQQLSOKLCTLAWSAHLVGHMDLREEG 60

QY 61 DEETNDVPHIQCGDCDPQGLRDNQSQCFLQRIHQGLIFYEKLGSIDFTGEPSSLDPSP 120
DB 61 DEETNDVPHIQCGDCDPQGLRDNQSQCFLQRIHQGLIFYEKLGSIDFTGEPSSLDPSP 120

QY 121 V 121
DB 121 V 121

Search completed: June 20, 2006, 05:05:35
Job time : 133.055 secs

THIS PAGE BLANK (USP1U)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2006, 05:01:19 ; Search time 12.7636 Seconds
(without alignments)
334.012 Million cell updates/sec

Title: US-10-797-157-2

Perfect score: 189

Sequence: 1 MLGSRVALLLLPWTQGR.....QAFVAVARVFAHGAATLSP 189

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 96747 seqs, 22556637 residues

Word size : 1

Total number of hits satisfying chosen parameters: 96737

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	3.7	10	6	US-10-538-066-129
2	7	3.7	10	6	US-10-538-066-130
3	7	3.7	11	6	US-10-538-066-231
4	7	3.7	11	6	US-10-538-066-252
5	7	3.7	80	6	US-10-449-902-39340
6	7	3.7	151	6	US-10-953-349-34638
7	7	3.7	189	6	US-10-505-928-117
8	7	3.7	247	6	US-10-953-349-34568
9	7	3.7	279	6	US-10-953-349-4862
10	7	3.7	280	6	US-10-953-349-12686
11	7	3.7	282	6	US-10-953-349-4961
12	7	3.7	294	6	US-10-449-902-39265
13	7	3.7	330	6	US-10-953-349-12685
14	7	3.7	331	6	US-10-449-902-37345
15	7	3.7	333	6	US-10-953-349-4960
16	7	3.7	361	6	US-10-953-349-12684
17	7	3.7	361	6	US-10-449-902-45582
18	7	3.7	394	6	US-10-538-066-754
19	7	3.7	439	6	US-10-449-902-47840
20	7	3.7	463	7	US-10-196-749-286
21	7	3.7	463	7	US-11-101-316-86
22	7	3.7	491	6	US-10-471-571A-1422
23	7	3.7	520	6	US-10-449-902-53256
24	7	3.7	629	6	US-10-449-902-34767
25	7	3.7	629	6	US-10-449-902-51918

26	7	3.7	653	6	US-10-953-349-11785
27	7	3.7	662	6	US-10-953-349-11784
28	7	3.7	684	6	US-10-953-349-11783
29	7	3.7	702	6	US-10-538-066-363
30	7	3.7	818	6	US-10-471-571A-3438
31	6	3.2	10	6	US-10-538-066-249
32	6	3.2	16	7	US-11-257-581-13
33	6	3.2	26	7	US-11-154-977-79
34	6	3.2	29	1	US-09-949-925-279
35	6	3.2	29	1	US-10-449-902-28491
36	6	3.2	40	6	US-10-449-902-39700
37	6	3.2	44	6	US-10-953-349-9223
38	6	3.2	47	7	US-11-156-014A-29
39	6	3.2	48	6	US-10-518-472-11
40	6	3.2	53	7	US-11-154-977-73
41	6	3.2	57	6	US-10-953-349-35581
42	6	3.2	58	1	US-09-949-925-193
43	6	3.2	60	6	US-10-449-902-44672
44	6	3.2	66	6	US-10-449-902-33763
45	6	3.2	77	6	US-10-449-902-34641

ALIGNMENTS

RESULT 1
US-10-538-066-129
; Sequence 129, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; TITLE OF INVENTION: Peptides and Compositions
; FILE REFERENCE: 2060.015PC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 129
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-538-066-129

Query Match 3.7%; Score 7; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 PWQRLLLL 161
DB 2 PWQRLLLL 8

RESULT 2
US-10-538-066-130
; Sequence 130, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; TITLE OF INVENTION: Peptides and Compositions
; FILE REFERENCE: 2060.015PC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 130
; LENGTH: 10
; TYPE: PRT

```
; ORGANISM: Homo sapiens
US-10-538-066-130

Query Match      3.7%   Score 7;   DB 6;   Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches      7;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY  155 PWQRLLL 161
    |||||
Db   2  PWQRLLL 8

RESULT 3
US-10-538-066-251
; Sequence 251, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; FILE REFERENCE: 2060.015PC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 251
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-538-066-251

Query Match      3.7%   Score 7;   DB 6;   Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches      7;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY  155 PWQRLLL 161
    |||||
Db   5  PWQRLLL 11

RESULT 4
US-10-538-066-252
; Sequence 252, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; FILE REFERENCE: 2060.015PC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 252
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-538-066-252

Query Match      3.7%   Score 7;   DB 6;   Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches      7;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY  155 PWQRLLL 161
    |||||
Db   1  PWQRLLL 7

RESULT 5
```

```
US-10-449-902-39340
; Sequence 39340, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39340
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-39340

Query Match      3.7%   Score 7;   DB 6;   Length 80;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches      7;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY  21 AVPGSS 27
    |||||
Db  18 AVPGSS 24

RESULT 6
US-10-953-349-34638
; Sequence 34638, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34638
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-34638

Query Match      3.7%   Score 7;   DB 6;   Length 151;
Best Local Similarity 100.0%; Pred. No. 17;
Matches      7;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY  57 REEGDEE 63
    |||||
Db  11 REEGDEE 17

RESULT 7
US-10-505-928-117
; Sequence 117, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
```

; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 117
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-117

Query Match 3.7%; Score 7; DB 6; Length 189;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 VMLLLL 13
| | | | |
Db 2 VMLLLLL 8

RESULT 8

US-10-953-349-34568
; Sequence 34568, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34568
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-34568

Query Match 3.7%; Score 7; DB 6; Length 247;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 PGGSSPA 29
| | | | |
Db 30 PGGSSPA 36

RESULT 9

US-10-953-349-4962
; Sequence 4962, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4962
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-4962

Query Match 3.7%; Score 7; DB 6; Length 279;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 MLLLLL 14
| | | | |
Db 188 MLLLLL 194

RESULT 10

US-10-953-349-12686
; Sequence 12686, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12686
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-12686

Query Match 3.7%; Score 7; DB 6; Length 280;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 MLLLLL 14
| | | | |
Db 189 MLLLLL 195

RESULT 11

US-10-953-349-4961
; Sequence 4961, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4961
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-4961

Query Match 3.7%; Score 7; DB 6; Length 282;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 MLLLLL 14
| | | | |
Db 191 MLLLLL 197

RESULT 12

US-10-449-902-39265
; Sequence 39265, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11

; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39265
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-39265

Query Match 3.7%; Score 7; DB 6; Length 294;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 176 AARVFAH 182
Db 158 AARVFAH 164
|||||

RESULT 13
US-10-953-349-12685
; Sequence 12685, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12685
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-12685

Query Match 3.7%; Score 7; DB 6; Length 330;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 MLLLLLP 14
Db 239 MLLLLLP 245
|||||

RESULT 14
US-10-449-902-37345
; Sequence 37345, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37345
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-37345

Query Match 3.7%; Score 7; DB 6; Length 331;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 57 REEGDEE 63
Db 312 REEGDEE 318
|||||

RESULT 15
US-10-953-349-4960
; Sequence 4960, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4960
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-4960

Query Match 3.7%; Score 7; DB 6; Length 333;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 MLLLLLP 14
Db 242 MLLLLLP 248
|||||

Search completed: June 20, 2006, 05:06:07
Job time : 13.7636 secs